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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 27.3926 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294a-51

Perfect score: 90
Sequence: 1 ISITRIKGVIRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_290a04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	90	100.0	19 6 AAB35657	Aae35657 Measles v
2	90	100.0	30 6 AAB35677	Aae35677 Human Abe
3	90	100.0	31 7 ADD89946	Add89946 CD4 pepti
4	90	100.0	32 6 AAB35678	Aae35678 Human Abe
5	90	100.0	34 6 AAB35679	Aae35679 Human Abe
6	90	100.0	45 7 ADD89951	Add89951 I95 pepti
7	90	100.0	48 6 AAB35680	Aae35680 Human Abe
8	90	100.0	50 7 ADD89944	Add89944 CD4 pepti
9	87	96.7	65 7 ADD89953	Add89953 Foot-and-
10	83	92.2	65 7 ADD89952	Add89952 Foot-and-
11	76	84.4	19 3 AAY68551	Aay68551 Helper T
12	76	84.4	19 3 AAY91135	Aay91135 Modified
13	76	84.4	19 5 ABG68202	ABg68202 Measles v
14	76	84.4	19 5 ABG68208	ABg68208 Measles v
15	76	84.4	19 6 AAB35653	Aae35653 Measles v
16	76	84.4	19 6 AAB35647	Aae35647 Measles v
17	76	84.4	19 6 AAE35644	Aae35644 Measles v
18	76	84.4	29 3 AAY91264	Aay91264 Modified
19	76	84.4	29 3 AAY91260	Aay91260 Modified
20	76	84.4	29 3 AAY91266	Aay91266 Modified
21	76	84.4	29 3 AAY91258	Aay91258 Modified
22	76	84.4	30 3 AAY91262	Aay91262 Modified
23	76	84.4	30 5 ABG68233	ABg68233 Optimised
24	76	84.4	31 3 AAY68582	Aay68582 Peptide 1
25	76	84.4	31 3 AAY91173	Aay91173 Modified

26	76	84.4	31 3 AAY91268	Aay91268 Modified
27	76	84.4	32 5 ABG68235	ABg68235 Optimised
28	76	84.4	34 5 ABG68231	ABg68231 Optimised
29	76	84.4	34 6 AAB35681	Aae35681 Human Abe
30	76	84.4	35 3 AAY91242	Aay91242 Modified
31	76	84.4	36 3 AAY91224	Aay91224 Modified
32	76	84.4	36 3 AAY91234	Aay91234 Modified
33	76	84.4	36 3 AAY91238	Aay91238 Modified
34	76	84.4	39 5 ABG68237	ABg68237 Optimised
35	76	84.4	46 3 AAY91240	Aay91240 Modified
36	76	84.4	46 3 AAY91213	Aay91213 Modified
37	76	84.4	46 3 AAY91232	Aay91232 Modified
38	76	84.4	46 3 AAY80020	Aay80020 I95 Immun
39	76	84.4	46 5 ABG68229	ABg68229 Optimised
40	76	84.4	46 5 ABG68227	ABg68227 Optimised
41	76	84.4	47 3 AAY68583	Aay68583 Peptide 1
42	76	84.4	47 3 AAY91180	Aay91180 Inv epit
43	76	84.4	49 3 AAY91177	Aay91177 Modified
44	76	84.4	51 3 AAY91248	Aay91248 Modified
45	76	84.4	52 3 AAY91270	Aay91270 Modified

ALIGNMENTS

RESULT 1
AAB35657 standard; peptide: 19 AA.
ID AAB35657
AC AAB35657;
DT 17-JUN-2003 (first entry)
XX
DE Measles virus T helper cell epitope #31.
XX
XX Immunogen: helper T cell, Th epitope; amyloid beta; Alzheimer's disease;
KM Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KM vaccine; nootropic.
XX
OS Measles virus.
XX
XX MO200296350-A2.
XX
XX 05-DEC-2002.
XX
XX 02-APR-2002; 2002MO-US010293.
XX
XX 25-MAY-2001; 2001US-00865294.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY;
XX
XX WPI; 2003-201258/19.
XX
XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
XX Claim 1; Page 37; 77pp; English.
XX
XX The present invention relates to a novel peptide immunogen comprising a
XX helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
XX (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
XX spacer consisting of at least an amino acid to separate the immunogenic
XX domains. Sequences of the invention are useful for preventing or treating
XX Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
XX peptide that is cross-reactive to soluble Abeta peptides and brain tissue
XX plaques formed from it. They are useful for eliciting a site-directed
XX mutagenesis against the main functional/regulatory site of the Abeta
XX peptide and for generating antibodies, which are highly cross-reactive to
XX the soluble Abeta peptide and the amyloid plaques formed in the brain of
XX Alzheimer's disease patients. The sequences are useful for induction of

CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention
SQ Sequence 19 AA;

Query Match 100.0%; Score 90; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITEIKGVYVRIETILF 19
1 ISITEIKGVYVRIETILF 19
Db

RESULT 2
ID AAE35677 standard; peptide; 30 AA.
AAE35677;

AC 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.
XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KM Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KV vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

OS Homo sapiens.
OS Measles virus.
OS Chimeric.

Key Location/Qualifiers
FH Region 1..10
FT /note="Human beta amyloid peptide"
FT Region 14..30
FT /note="Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PS Claim 9; Page 39; 77pp; English.

CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of

CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 30 AA;

Query Match 100.0%; Score 90; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITEIKGVYVRIETILF 19
12 ISITEIKGVYVRIETILF 30
Db

RESULT 3
ID ADD89946 standard; protein; 31 AA.
ADD89946;

AC ADD89946;
DT 29-JAN-2004 (first entry)

DE CD4 peptide used in immunostimulant complex for anti-HIV vaccine.

XX Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.

XX Synthetic.

OS Homo sapiens.

Key Location/Qualifiers
FH Modified-site 20
FT /note="Epsilon-lysine"

XX WO2003068169-A2.

XX 21-AUG-2003.

XX 14-FEB-2003; 2003WO-US004711.

XX 14-FEB-2002; 2002US-00076674.

XX 31-JAN-2003; 2003US-00076674.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Sokoll KK;

XX WPI; 2003-778890/73.

PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.

PS Claim 14; SEQ ID NO 6; 159pp; English.

CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human CD4. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a Cpg oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to Cpg oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present CD4 derived peptide can be used in an anti-
CC CD4 immunotherapeutic vaccine for the treatment of HIV infection.

SQ Sequence 31 AA;

Query Match 100.0%; Score 90; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITRIKGVVRIETILF 19
1 ISITRIKGVVRIETILF 19
Db

RESULT 4
AAE35678
ID AAE35678 standard; peptide; 32 AA.

AC AAE35678;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..12 /note= "Human beta amyloid peptide"

FT Region 16..32 /note= "Measles virus T helper cell epitope"

FT Region

FN MO200296350-A2.

PD 05-DEC-2002.

PF 02-APR-2002; 2002MO-US010293.

PR 25-MAY-2001; 2001US-00865294.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2003-201258/19.

PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PS Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domain. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 90; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITRIKGVVRIETILF 19
14 ISITRIKGVVRIETILF 32
Db

RESULT 5
AAE35679

ID AAE35679 standard; peptide; 34 AA.

AC AAE35679;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..14 /note= "Human beta amyloid peptide"

FT Region 18..34 /note= "Measles virus T helper cell epitope"

FT Region

FN MO200296350-A2.

PD 05-DEC-2002.

PF 02-APR-2002; 2002MO-US010293.

PR 25-MAY-2001; 2001US-00865294.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2003-201258/19.

PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PS Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domain. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope

CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 90; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISTEIKGVVRIETILF 19
|||
16 ISTEIKGVVRIETILF 34

Db

RESULT 6
ADD89951
ID ADD89951 standard; protein; 45 AA.
XX
AC ADD89951;
XX

DT 29-JAN-2004 (first entry)

DE IGB peptide used in immunostimulant complex for allergy vaccine.

XX Immunostimulant; vaccine; human; immunogen; IGB; immunotherapy; allergy;
KM antibody; anti-allergic.

XX Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers
FT Modified-site 20
/note= "Epsilon-lysine"

PN W02003068169-A2.

XX 21-AUG-2003.

PD 14-FEB-2003; 2003WO-US0047711.

XX 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Sokol KR;

DR MPI; 2003-778890/73.

XX Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.

PS Claim 20; SEQ ID NO 11; 159pp; English.

XX The present sequence is that of a synthetic immunogenic peptide derived
CC from human IGB. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a Cpg oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to Cpg oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present IGB derived peptide can be used in an anti
CC -IGB immunotherapeutic vaccine for the treatment of allergy.

XX Sequence 45 AA;

Query Match 100.0%; Score 90; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISTEIKGVVRIETILF 19
|||
1 ISTEIKGVVRIETILF 19

Db

RESULT 7
AAE35680
ID AAE35680 standard; peptide; 48 AA.

XX AAE35680;

DT 23-OCT-2003 (revised)

DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KM Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KM vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers
FT Region 1..28 "Human beta amyloid peptide"
FT Region 32..48
/note= "Measles virus T helper cell epitope"

PN W0200296350-A2.

PD 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA Wang CY;

DR MPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PS Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of the
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 48 AA;

Query Match 100.0%; Score 90; DB 6; Length 48;

Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ISITIKGVVHRIETILF 19
DB 30 ISITIKGVVHRIETILF 48

RESULT 8

ADD89944 standard; protein; 50 AA.

AC ADD89944;

DT 29-JAN-2004 (first entry)

DE CD4 peptide used in immunostimulant complex as anti-HIV vaccine.

KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 20 /note="Epsilon-lysine"

PN W02003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

DR WPI; 2003-778890/73.

CC Stabilized immunostimulating complex, useful for vaccination, e.g.

PT against human immune deficiency viruses, comprises cationic peptide

PT immunogen and anionic oligonucleotide.

PS Claim 14; SEQ ID NO 4; 159pp; English.

CC The present sequence is that of a synthetic immunogenic peptide derived

CC from human CD4. This is an example of peptides that can be used in

CC claimed immunostimulatory complexes of the invention that are

CC specifically adapted to act as adjuvant and as peptide immunogen

CC stabiliser. The complexes comprise a CpG oligonucleotide and a

CC biologically active peptide immunogen. The complex is particulate and can

CC efficiently present peptide immunogens to the cells of the immune system

CC to produce an immune response. The complexes may be prepared with various

CC ratios of peptides to CpG oligonucleotides to provide different physical

CC properties, such as the size of the microparticle. An immunostimulatory

CC complex comprising the present CD4 derived peptide can be used in an anti

CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection.

CC SQ Sequence 50 AA;

Query Match 100.0%; Score 90; DB 7; Length 50;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISITIKGVVHRIETILF 19

DB 1 ISITIKGVVHRIETILF 19

RESULT 9

ADD89953 standard; protein; 65 AA.

AC ADD89953;

DT 29-JAN-2004 (first entry)

DE Foot-and-mouth disease peptide used in vaccine immunostimulant complex.

KW Immunostimulant; vaccine; immunogen; immunotherapy;

KW Foot-and-mouth disease.

OS Synthetic.

OS Foot-and-mouth disease virus.

FT Key Location/Qualifiers

FT Modified-site 20 /note="Epsilon-lysine"

PN W02003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

DR WPI; 2003-778890/73.

CC Stabilized immunostimulating complex, useful for vaccination, e.g.

PT against human immune deficiency viruses, comprises cationic peptide

PT immunogen and anionic oligonucleotide.

PS Claim 22; SEQ ID NO 13; 159pp; English.

CC The present sequence is that of a synthetic immunogenic peptide derived

CC from foot-and-mouth disease (FMD) virus. This is an example of peptides

CC that can be used in claimed immunostimulatory complexes of the invention

CC that are specifically adapted to act as adjuvant and as peptide immunogen

CC stabiliser. The complexes comprise a CpG oligonucleotide and a

CC biologically active peptide immunogen. The complex is particulate and can

CC efficiently present peptide immunogens to the cells of the immune system

CC to produce an immune response. The complexes may be prepared with various

CC ratios of peptides to CpG oligonucleotides to provide different physical

CC properties, such as the size of the microparticle. An immunostimulatory

CC complex comprising the present FMD virus derived peptide can be used in

CC an anti-FMD vaccine for protective immunity against FMD.

CC SQ Sequence 65 AA;

Query Match 96.7%; Score 87; DB 7; Length 65;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISITIKGVVHRIETILF 19

DB 1 ISITIKGVVHRIETILF 19

RESULT 10

ADD89952 standard; protein; 65 AA.

AC ADD89952;

DT 29-JAN-2004 (first entry)

DE Foot-and-mouth disease peptide used in vaccine immunostimulant complex.

XX		Immunostimulant; vaccine; immunogen; immunoherapy;
KW		foot-and-mouth disease.
OS	Synthetic.	
OS	Foot-and-mouth disease virus.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site	/note= "Epsilon-lysine"
PT	20	
XX		
PV	WO2003068169-A2.	
PN		
PD	21-Aug-2003.	
PP	14-FEB-2003; 2003WO-US004711.	
PR	14-FEB-2002; 2002US-00076674.	
PR	31-JAN-2003; 2003US-00076674.	
PA	(UNBI-) UNITED BIOMEDICAL INC.	
XK	Sokol I KK;	
PI		
DR	WI; 2003-778890/73.	
XX		
PT	Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.	
PS	Claim 22; SEQ ID NO 12; 159pp; English.	
CC	The present sequence is that of a synthetic immunogenic peptide derived from foot-and-mouth disease (FMD) virus. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogens to the cells of the immune system to produce an immune response. The complexes may be prepared with various ratios of peptides to CpG oligonucleotides to provide different physical properties, such as the size of the microparticle. An immunostimulatory complex comprising the present FMD virus derived peptide can be used in an anti-FMD vaccine for protective immunity against FMD.	
CC		
CC		
CC	Sequence 65 AA;	
SQ		
OY	Query Match	92.2%; Score 83; DB 7; Length 65;
pb	Best Local Similarity	89.5%; Pred No. 8.5e-07;
	Matches 17; Conservative	2; Mismatches 0; Indels 0; Gaps 0
	1 ISITEIKGVIVRIETILP 19	
	: :	
	1 ISISIEIKGVIVRIETILP 19	
RESULT 11		
AAY68551	AAI68551 standard; peptide; 19 AA.	
AC	AAY68551;	
XX		
DT	05-MAY-2000 (first entry)	
DB	Helper T cell epitope derived from SSAL Th1.	
XX		
KW	Structured synhtetic antigen library; SSAL; helper T cell epitope; SSAL Th1; P protein; Measles virus; peptide immunogen; LHRH; luteinising hormone-releasing hormone; spermatogenesis; ovulation; oestrus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; immunocastration.	

OS	Synthetic.
OS	Measles virus.
FN	MO3966952-A1.
PD	29-DEC-1999.
PE	21-JUN-1999; 99WO-US0133960.
PR	20-JUN-1998; 98US-00100414.
PA	(UNBI-) UNITED BIOMEDICAL INC.
PX	Wang CY;
DR	WP1; 2000-160562/14.
PT	New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
PS	Claim 1; Page 29; 102pp; English.
CC	The present sequence represents a helper T cell epitope derived from a structured synthetic antigen library (SSAL) helper T cell epitope designated SSAL1.Th1. SSAL.Th1 is modelled after a promiscuous epitope taken from the P protein of the Measles virus. The present epitope is designed to be used in tandem with a target antigen, luteinizing hormone-releasing hormone (LHRH). The epitope is used to construct peptide immunogens of the invention, which contain at least one antigenic target site, i.e. luteinizing hormone-releasing hormone (LHRH) or its analogue, and an artificial helper T cell epitope (Th). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosist); to prevent boar taint (and improve meat quality) and for immunocastration
SC	Sequence 19 AA:
QY	Query Match 84.4%; Score 76; DB 3; Length 19; Best Local Similarity 84.2%; Pred. No. 3e-06; Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cy	1 ISITRIKGVIVRHRIETLP 19 : : : 1 ISITRIKGVIVKHIGILP 19
Db	RESULT 12 ID AAY91135 standard; peptide; 19 AA. AAY91135 AAY91135; 22-MAY-2000 (first entry)
DE	Modified measles virus F protein promiscuous Th epitope, SEQ ID NO:15.
KM	Promiscuous T-cell epitope; measles virus F protein; MVR;
KM	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM	luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
KM	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
KM	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM	Plasmodium falciparum; circumsporozoite; antimalarial; CPTP;
KM	cholesterol ester transport protein; anti-arteriosclerotic.
OS	Measles virus.

OS Synthetic.
 XX NO996957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US013975.
 XX
 PR 20-JUN-1998; 98US-00100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus.
 XX
 PS Claim 1; Page 54; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response.
 CC Specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and immunocastration
 CC ; for promoting the growth of animals; or for treating allergies or
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
 CC genetically diverse subjects) into an immunogen improves capacity to
 CC induce a strong T helper cell-mediated immune response, resulting in
 CC production of antibodies against a target antigen. Th can replace carrier
 CC proteins and pathogen-derived T helper epitopes. Sequence AA191121
 CC represents a promiscuous T helper epitope from the measles virus F (MVF)
 CC protein and sequences AA191122-Y91142, AA191226 and AA191245-Y91246
 CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
 CC AA191143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
 CC surface antigen, and sequences AA191144-Y91155 are synthetic epitopes
 CC derived from this HBV epitope. AA191156-Y91196, AA191227 and AA191242-
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
 CC promiscuous Th epitope. AA191197 is the LHRH target antigenic peptide
 CC used in these LHRH antigenic peptides. AA191200 is somatostatin, and
 CC AA191201-Y91207 are antigenic peptides comprising somatostatin and a Th
 CC epitope. Somatostatin immunogens may be used to promote growth in
 CC livestock. AA191208 is a human CD4 CDR2-like domain antigenic site, and
 CC AA191209-Y91211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
 CC be used to prevent HIV infection of T cells. AA191212 is a modified
 CC version of a human IGB (immunoglobulin B) CH3 domain, and AA191213-Y91219
 CC are Th epitope/IGB CH3 antigenic peptides which may be used in the
 CC treatment of allergies. AA191220 is a peptide derived from foot and mouth
 CC disease virus (FMDV) VP1 capsid protein and AA191221-Y91222 comprise this
 CC peptide and a Th epitope. AA191223 is a Plasmodium falciparum
 CC circumsporozoite (CS) target antigen, and AA191224-Y91225 comprise the CS
 CC antigen and an MWP Th epitope and may be used in a malaria vaccine.
 CC AA191228-Y91231 represent CEP-derived peptides and AA191232-Y91241 are
 CC immunogens comprising a CEP peptide and a Th epitope which may be used
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AA191247
 CC and AA191252-Y91257 are HIV-1 neutralising B-cell epitopes, and AA191248-
 CC Y91251 and AA191258-Y91273 are antigenic peptides comprising MVH Th and
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
 CC vaccine. AA191198 and AA191199 are respectively an immunostimulatory
 CC invasion protein epitope from Yersinia species, and hinge spacer peptide,
 CC both of which may optionally be used in the antigenic peptides of the
 CC invention
 XX
 SQ Sequence 19 AA;

Query Match 84.4%; Score 76; DB 3; Length 19;
 Best Local Similarity 84.2%; Pred. No. 3e-06;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISITIKGVYHRIETLP 19
 |||:|||||:|||||
 Db 1 ISISIKGVYHRIETLP 19

RESULT 13
 ABG68202

ID ABG68202 standard; peptide; 19 AA.

AC ABG68202;

DT 07-OCT-2002 (first entry)

DE Measles virus idealised helper T cell epitope #20.

KW Immunogen; FimH adhesin functional site-derived target peptide; FAFSD;

KW helper T cell epitope; FimH; urinary tract infection;

KW type 1 fimbriated uropathogenic enterobacteria; vaccine;

KW FAFSD site-specific immunity; measles virus.

OS Measles virus.

XX Synthetic.

FM WO200251860-A2.

PD 04-JUL-2002.

PP 21-DEC-2001; 2001WO-US050816.

PR 22-DEC-2000; 2000US-00747802.

PA (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

DR WPI; 2002-528681/56.

PT Novel peptide immunogen, useful for evoking antibodies to prevent
 PT adherence of Escherichia coli to bladder mucosa, comprises a FimH
 PT functional site-derived target peptide covalently linked to helper T cell
 PT epitope.

PS Claim 18; Page 8; 62pp; English.

CC The invention describes a peptide immunogen (I), comprising a helper T
 CC cell epitope sequence (Th) or a carrier protein covalently attached to a
 CC FimH adhesin functional site-derived (FAFSD) target peptide comprising
 CC not more than 30 amino acids of the carbohydrate binding pocket of FimH,
 CC or its crossreactive and immunologically functional analogue or mimotope.
 CC (I) and a composition containing (I) are useful for inducing anti-FAFSD
 CC peptide antibody production in a mammal. The composition is also useful
 CC for reducing adherence to the urinary tract mucosa of a mammal by type 1
 CC fimbriated uropathogenic enterobacteria (Escherichia coli) to prevent
 CC urinary tract infection. (I) has a focused FAFSD site-specific immunity
 CC together with a broad protective immunity, and with less adverse side
 CC reactions than the more complex polypeptide subunit vaccines and the
 CC carrier conjugated vaccine. Since (I) is chemically well defined it is
 CC easy and less costly to manufacture and to control or assure the quality
 CC of the product. This sequence represents a helper T cell epitope derived
 CC from the measles virus used in the creation of a vaccine against urinary
 CC tract infection
 CC
 XX

SQ Sequence 19 AA;

Query Match 84.4%; Score 76; DB 5; Length 19;

Best Local Similarity 84.2%; Pred. No. 3e-06;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 7.46012 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-51

Perfect score: 90
Sequence: 1 ISITRIKGVIVRIETILP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents: AA:*
1: /cgn2_6/pdata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/pdata/2/1aa/backlitest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	84.4	19	3	US-09-100-414B-15
2	76	84.4	19	3	US-09-303-323-15
3	76	84.4	19	4	US-09-770-014-15
4	76	84.4	31	3	US-09-100-414B-53
5	76	84.4	31	3	US-09-303-323-53
6	76	84.4	31	4	US-09-770-014-53
7	76	84.4	35	3	US-09-100-414B-80
8	76	84.4	35	3	US-09-303-323-80
9	76	84.4	35	4	US-09-770-014-80
10	76	84.4	46	3	US-09-100-414B-96
11	76	84.4	46	3	US-09-303-323-96
12	76	84.4	46	4	US-09-770-014-96
13	76	84.4	47	3	US-09-100-414B-60
14	76	84.4	47	4	US-09-303-323-60
15	76	84.4	47	4	US-09-770-014-60
16	76	84.4	49	3	US-09-100-414B-57
17	76	84.4	49	3	US-09-303-323-57
18	76	84.4	49	4	US-09-770-014-57
19	76	84.4	80	3	US-09-100-600A-30
20	76	84.4	19	3	US-09-100-414B-17
21	76	84.4	19	3	US-09-303-323-17
22	76	84.4	19	4	US-09-770-014-17
23	76	84.4	31	3	US-09-100-414B-55
24	76	84.4	31	3	US-09-303-323-55
25	76	84.4	31	4	US-09-770-014-55
26	76	84.4	19	3	US-09-100-414B-18
27	76	84.4	19	3	US-09-100-414B-19

28	69	76.7	19	3	US-09-100-414B-20	Sequence 20, Appl
29	69	76.7	19	3	US-09-303-323-18	Sequence 18, Appl
30	69	76.7	19	3	US-09-303-323-19	Sequence 19, Appl
31	69	76.7	19	3	US-09-303-323-20	Sequence 20, Appl
32	69	76.7	19	4	US-09-770-014-18	Sequence 18, Appl
33	69	76.7	19	4	US-09-770-014-19	Sequence 19, Appl
34	69	76.7	19	4	US-09-770-014-20	Sequence 20, Appl
35	69	76.7	31	3	US-09-100-414B-56	Sequence 56, Appl
36	69	76.7	31	3	US-09-100-414B-59	Sequence 59, Appl
37	69	76.7	31	3	US-09-100-414B-61	Sequence 61, Appl
38	69	76.7	31	3	US-09-303-323-56	Sequence 56, Appl
39	69	76.7	31	3	US-09-303-323-59	Sequence 59, Appl
40	69	76.7	31	3	US-09-303-323-61	Sequence 61, Appl
41	69	76.7	31	4	US-09-770-014-56	Sequence 56, Appl
42	69	76.7	31	4	US-09-770-014-59	Sequence 59, Appl
43	69	76.7	31	4	US-09-770-014-61	Sequence 61, Appl
44	69	76.7	35	3	US-09-100-414B-81	Sequence 81, Appl
45	69	76.7	35	3	US-09-303-323-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-15
; Sequence 15, Application US/09100414B
; Patent No. 6025468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LRRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flanagan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09100,414B

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: peptide

US-09-100-414B-15

Query Match 84.4%; Score 76; DB 3; Length 19;

Best Local Similarity 84.2%; Pred. No. 4.3e-07; Indels 0; Gaps 0;

Matches 16; Conservative 2; Mismatches 1;

QY 1 ISITRIKGVIVRIETILP 19

DB 1 ISITRIKGVIVRIETILP 19

RESULT 2

US-09-303-323-15
Sequence 15, Application US/09303323
Patent No. 6228887
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303.323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-15
Query Match 84.4%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.3e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ISITEIKGVYHRIETILF 19
DB 1 ISISIKGVYHRIETILF 19
RESULT 3
US-09-770-014-15
Sequence 15, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-758-4800
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-15
Query Match 84.4%; Score 76; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.3e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ISITEIKGVYHRIETILF 19
DB 1 ISISIKGVYHRIETILF 19
RESULT 4
US-09-100-414B-53
Sequence 53, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-758-4800
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-53
Query Match 84.4%; Score 76; DB 3; Length 31;
Best Local Similarity 84.2%; Pred. No. 7.7e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISTEIKGVIVHRTIIF 19
|||:|||||:|||||
DB 1 ISISEIKGVIVHRTIIF 19

RESULT 5

US-09-303-323-53
Sequence 53, Application US/09303323

Patent No. 6228987

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSER: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,323

FILING DATE: 30-APR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-303-323-53

Query Match 84.4%; Score 76; DB 3; Length 31;

Best Local Similarity 84.2%; Pred. No. 7.7e-07;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISTEIKGVIVHRTIIF 19
|||:|||||:|||||

DB 1 ISISEIKGVIVHRTIIF 19

RESULT 6

US-09-770-014-53

Sequence 53, Application US/09770014

Patent No. 6559282

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSER: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,014

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-770-014-53

Query Match 84.4%; Score 76; DB 4; Length 31;

Best Local Similarity 84.2%; Pred. No. 7.7e-07;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISTEIKGVIVHRTIIF 19
|||:|||||:|||||

DB 1 ISISEIKGVIVHRTIIF 19

RESULT 7

US-09-100-414B-80

Sequence 80, Application US/09100414B

Patent No. 6025468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSER: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,414B

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

US-09-100-414B-80

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-80

Query Match 84.4%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 8.9e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISITIKGVIVRIETILP 19
DB 1 ISISIKGVIVKIKIGILP 19

RESULT 8
US-09-303-323-80
Sequence 80, Application US/09303323

PATENT No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-80

Query Match 84.4%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 8.9e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISITIKGVIVRIETILP 19
DB 1 ISISIKGVIVKIKIGILP 19

RESULT 9
US-09-770-014-80
Sequence 80, Application US/09770014

PATENT No. 6553282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-80

Query Match 84.4%; Score 76; DB 4; Length 35;
Best Local Similarity 84.2%; Pred. No. 8.9e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISITIKGVIVRIETILP 19
DB 1 ISISIKGVIVKIKIGILP 19

RESULT 10
US-09-100-414B-96
Sequence 96, Application US/09100414B

PATENT No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 84.4%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 1.2e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISITIKGVIVHRIETILP 19
Db 1 ISISIKGVIVHRIETILP 19

RESULT 11

US-09-303-323-96
Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-96

Query Match 84.4%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 1.2e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISITIKGVIVHRIETILP 19
Db 1 ISISIKGVIVHRIETILP 19

RESULT 12

US-09-770-014-96
Sequence 96, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-96

Query Match 84.4%; Score 76; DB 4; Length 46;
Best Local Similarity 84.2%; Pred. No. 1.2e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISITIKGVIVHRIETILP 19
Db 1 ISISIKGVIVHRIETILP 19

RESULT 13

US-09-100-414B-60
Sequence 60, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 71
LENGTH: 30
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-71

Query Match 100.0%; Score 90; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISITIKGVVRIETILF 19
|||
DB 12 ISITIKGVVRIETILF 30

RESULT 3

US-10-076-674-6
Sequence 6, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

Query Match 100.0%; Score 90; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISITIKGVVRIETILF 19
|||
DB 1 ISITIKGVVRIETILF 19

RESULT 4

US-10-355-161A-6
Sequence 6, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

Query Match 100.0%; Score 90; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISITIKGVVRIETILF 19
|||
DB 1 ISITIKGVVRIETILF 19

RESULT 5

US-09-865-294-72
Sequence 72, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 32
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-72

Query Match 100.0%; Score 90; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISITIKGVVRIETILF 19
|||
DB 14 ISITIKGVVRIETILF 32

RESULT 6

US-09-865-294-73
Sequence 73, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 34
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-73

Query Match 100.0%; Score 90; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISITIKGVVRIETILF 19
|||
DB 16 ISITIKGVVRIETILF 34

RESULT 7

US-10-076-674-11
Sequence 11, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System

CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

Query Match 100.0%; Score 90; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITBIKGVIVHRIETILF 19
Db 1 ISITBIKGVIVHRIETILF 19

RESULT 8
US-10-355-161A-11
Sequence 11, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

Query Match 100.0%; Score 90; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITBIKGVIVHRIETILF 19
Db 1 ISITBIKGVIVHRIETILF 19

RESULT 9
US-09-865-294-74
Sequence 74, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
prevention of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 74
LENGTH: 48
TYPE: PRT
ORGANISM: Measles virus

US-09-865-294-74

Query Match 100.0%; Score 90; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITBIKGVIVHRIETILF 19
Db 30 ISITBIKGVIVHRIETILF 48

RESULT 10
US-10-076-674-4
Sequence 4, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 50
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

Query Match 100.0%; Score 90; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITBIKGVIVHRIETILF 19
Db 1 ISITBIKGVIVHRIETILF 19

RESULT 11
US-10-355-161A-4
Sequence 4, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 50
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

Query Match 100.0%; Score 90; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITBIKGVIVHRIETILF 19
Db 1 ISITBIKGVIVHRIETILF 19

```
RESULT 12
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

Query Match          96.7%; Score 87; DB 15; Length 65;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ISITIKGIVHRIETILF 19
   |||:|||||:|||||
Db 1 ISITIKGIVHRIETILF 19

RESULT 13
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

Query Match          92.2%; Score 83; DB 15; Length 65;
Best Local Similarity 89.5%; Pred. No. 6.9e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ISITIKGIVHRIETILF 19
   |||:|||||:|||||
Db 1 ISITIKGIVHRIETILF 19

RESULT 14
US-09-747-802-49
; Sequence 49, Application US/09747802
; Publication No. US20030027979A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHANG YI
; TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
; FILE REFERENCE: PREVENTION OF URINARY TRACT INFECTION
; CURRENT APPLICATION NUMBER: US/09/747,802
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 49
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T HELPER
US-09-747-802-49

Query Match          84.4%; Score 76; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.6e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ISITIKGIVHRIETILF 19
   |||:|||||:|||||
Db 1 ISITIKGIVHRIETILF 19

RESULT 15
US-09-747-802-55
; Sequence 55, Application US/09747802
; Publication No. US20030027979A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHANG YI
; TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
; FILE REFERENCE: PREVENTION OF URINARY TRACT INFECTION
; CURRENT APPLICATION NUMBER: US/09/747,802
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T HELPER
US-09-747-802-55

Query Match          84.4%; Score 76; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.6e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ISITIKGIVHRIETILF 19
   |||:|||||:|||||
Db 1 ISITIKGIVHRIETILF 19
```

Search completed: June 18, 2004, 20:23:46
Job time : 21.4479 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 5.7166 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-51

Perfect score: 90
Sequence: 1 SITRIKGVIVRIETLIF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: PIR 78: *
2: p1r1: *
3: p1r2: *
4: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	71.1	546	1 VGNZRL	cell fusion glycop
2	61	67.8	546	2 S47300	gene F protein - r
3	60	66.7	546	1 VGNZRL	cell fusion glycop
4	60	66.7	546	2 S55386	cell fusion protei
5	60	66.7	546	2 S47305	gene F protein - r
6	59	65.6	542	2 JQ2223	cell fusion protei
7	59	65.6	552	2 S47034	cell fusion protei
8	59	65.6	662	1 VGNZCD	cell fusion glycop
9	59	65.6	662	2 S21382	cell fusion protei
10	58	64.4	282	2 PQ0376	cell fusion glycop
11	58	64.4	282	2 PQ0388	cell fusion glycop
12	58	64.4	534	1 JU0274	cell fusion glycop
13	58	64.4	550	1 E48556	cell fusion glycop
14	58	64.4	553	1 VGNZMV	cell fusion glycop
15	58	64.4	631	1 VGNZPD	cell fusion glycop
16	58	64.4	631	1 A48346	cell fusion glycop
17	48	53.3	220	2 T00801	probable synaptochr
18	48	53.3	229	2 P86180	probable synaptochr
19	47	52.2	240	2 T47589	synaptochrvin-like
20	45	50.0	451	2 AH0063	conserved hypochet
21	45	50.0	636	2 S47299	gene F protein - r
22	44	48.9	175	2 D86180	hypothetical prote
23	44	48.9	221	2 P84741	probable synaptochr
24	43	47.8	708	2 T43109	cytolysin B transp
25	42.5	47.2	531	2 B82295	translation releas
26	42	46.7	236	2 A90190	hypothetical prote
27	42	46.7	329	2 T33378	hypothetical prote
28	42	46.7	1246	2 T00826	hypothetical prote
29	42	46.7	1816	2 A84845	probable ABC trans

30 41.5 46.1 428 2 A82215 probable alanine r
31 41 45.6 244 2 T43566 translocation lipop
32 41 45.6 244 2 A40049 viC-region lipop
33 41 45.6 248 2 C83431 type III export pr
34 41 45.6 571 2 T38759 probable pyruvate
35 41 45.6 1140 2 S73786 hypothetical prote
36 41 45.6 2479 2 P87366 conserved hypochet
37 40 44.4 127 2 G69516 hypothetical prote
38 40 44.4 145 2 A10110 hypothetical prote
39 40 44.4 165 2 T27540 hypothetical prote
40 40 44.4 263 2 H69336 cell division inh
41 40 44.4 444 2 UC7084 alpha-1,3-mannosyl
42 40 44.4 456 2 B97129 probable metal-dep
43 40 44.4 457 2 T05651 hypothetical prote
44 40 44.4 565 1 VGNZSV cell fusion glycop
45 40 44.4 565 1 VGNZSH cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)

N:Contains: fusion glycoprotein P1, fusion glycoprotein P2

C:Species: rinderpest virus

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C:Accession: A28921

R:Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.

Virology 164, 523-530, 1988

A:Title: Fusion glycoprotein (P) of rinderpest virus: entire nucleotide sequence of the

A:Reference number: A28921; MUID:88219541; PMID:3285575

A:Accession: A28921

A:Molecule type: mRNA

A:Residues: 1-546 <TSU>

A:Cross-references: GB:M20870; NID:G333898; PIDN:AAA47399.1; PID:G333899

C:Genetic8:

A:Gene: P

C:Superfamily: paramfluenza virus cell fusion protein

C:Keywords: glycoprotein; membrane fusion; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-104/Product: cell fusion glycoprotein P2 #status predicted <PG2>

F:105-546/Product: cell fusion glycoprotein P1 #status predicted <PG1>

F:109-133/Domain: transmembrane #status predicted <TM1>

F:485-513/Domain: transmembrane #status predicted <TM2>

F:25-57.63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.1%; Score 64; DB 1; Length 546;

Best Local Similarity 61.1%; Pred. No. 0.0087;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SITRIKGVIVRIETLIF 19
Db 283 SITRIKGVIVRIETLIF 300

RESULT 2

S47300
gene F protein - rinderpest virus

C:Species: rinderpest virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999

C:Accession: S47300; PQ0865

R:Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.

submitted to the EMBL Data Library, March 1994

A:Description: The complete nucleotide sequence of the fusion protein gene of the vaccir

A:Reference number: S47299

A:Accession: S47300

A:Molecule type: DNA

A:Residues: 1-546 <EVA>

A:Cross-references: EMBL:231656; NID:G535406; PIDN:CAA83482.1; PID:G535407

R:Chamberlain, R.W.; Wamwayi, H.M.; Hockley, B.; Shalla, M.S.; Goatley, L.; Knowles, N.J.

J. Gen. Virol. 74, 2775-2780, 1993

A:Title: Evidence for different lineages of rinderpest virus reflecting their geographic

A;Reference number: PQ0865; MUID:94103786; PMID:8277286
A;Accession: PQ0865
A;Molecule type: mRNA
A;Residues: 86-191 <CHA>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein

Query Match 67.8%; Score 61; DB 2; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.028;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVYHRIETILF 19
DB 283 SLSEIKGVYHRIETILF 300

RESULT 3
VGNZRR
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete 0)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: A31051
R;Heu, D.; Yamana, M.; Miller, J.; Dale, B.; Grubman, M.; Ylma, T.
Virology 166, 149-153, 1988
A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis
A;Reference number: A31051; MUID:88322864; PMID:3413983
A;Accession: A31051
A;Molecule type: genomic RNA
A;Residues: 1-546 <HSU>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-108/Product: cell fusion glycoprotein F2 #status predicted <FP1>
F;109-546/Product: cell fusion glycoprotein F1 #status predicted <FP2>
F;109-134/Domain: transmembrane #status predicted <TN1>
F;491-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63,518/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 66.7%; Score 60; DB 1; Length 546;
Best Local Similarity 55.6%; Pred. No. 0.041;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVYHRIETILF 19
DB 283 SLSEIKGVYHRIETILF 300

RESULT 4
S55386
cell fusion protein - peste-des-petite-ruminants virus (strain 75/1)
N;Alternate names: F protein
C;Species: peste-des-petite-ruminants virus
A;Variety: strain 75/1
C;Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
C;Accession: S55386
R;Meyer, G.; Diallo, A.
submitted to the EMBL Data Library, September 1994
A;Description: The nucleotide sequence of fusion protein gene of the Peste des petits ruminants virus.
A;Reference number: S55386
A;Accession: S55386
A;Molecule type: DNA
A;Residues: 1-546 <MBY>
A;Cross-references: EMBL:Z37017; NID:9854372; PTDN:CA85451.1; PID:9854373
A;Experimental source: strain 75/1; cell line vero
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: membrane fusion

Query Match 66.7%; Score 60; DB 2; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.041;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVYHRIETILF 19
DB 283 SLSEIKGVYHRIETILF 300

RESULT 5
S47305
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
C;Accession: S47305, S47301
R;Baron, M.D.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The sequence of the N and L genes of Rinderpest virus, and the 50 and 30
A;Reference number: S47283
A;Accession: S47305
A;Molecule type: mRNA
A;Residues: 1-546 <BAR>
A;Cross-references: EMBL:Z30697; NID:9535396; PTDN:CA83181.1; PID:9535401; EMBL:Z30700
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: transmembrane protein

Query Match 66.7%; Score 60; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 0.041;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVYHRIETILF 19
DB 283 SLSEIKGVYHRIETILF 300

RESULT 6
JQ2223
cell fusion protein F0 precursor - phocine distemper virus
N;Contains: F1 and F2 chains
C;Species: phocine distemper virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-1999
C;Accession: JQ2223
J;Visser, I.K.G.; van der Heijden, R.W.J.; van de Bildt, M.W.G.; Kemler, M.J.H.; Oerel
J. Gen. Virol. 74, 1989-1994, 1993
A;Title: Fusion protein gene nucleotide sequence similarities, shared antigenic sites a
e virus entity.
A;Reference number: JQ2223; MUID:93389459; PMID:8376973
A;Accession: JQ2223
A;Molecule type: mRNA
A;Residues: 1-542 <VIS>
A;Cross-references: GB:L07075
A;Note: the authors translated the codon ATC for residue 4 as Leu
C;Comment: This fusion protein F0 is cleaved into F1 and F2 chains.
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-542/Product: fusion protein #status predicted <MAT>
F;16-99/Product: F2 chain #status predicted <F2C>
F;105-542/Product: F1 chain #status predicted <F1C>
F;105-135/Region: hydrophobic
F;486-512/Domain: transmembrane #status predicted <TM>
F;21,53,59,397/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 65.6%; Score 59; DB 2; Length 542;
Best Local Similarity 50.0%; Pred. No. 0.06;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVYHRIETILF 19
DB 283 SLSEIKGVYHRIETILF 300

DB 279 TLSEVKGIVHRLAVSY 296

RESULT 7

S47034
cell fusion protein precursor - porpoise morbillivirus
N:Alternate names: F protein
C:Species: Porpoise morbillivirus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S47034
R:Bolt, G.; Gottschalk, E.; Blikenkron-Neeller, M.; Wishaupt, R.G.A.; Welsh, M.J.; Ba
submitted to the EMBL Data Library, July 1994
A:Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbilli
A:Reference number: S47034
A:Accession: S47034
A:Molecule type: mRNA
A:Residues: 1-552 <BOL>
A:Cross-references: EMBL:X80757; NID:G520639; PIDN:CAA56731.1; PID:G520640
A:Experimental source: Isolate Ulster 88
A>Note: the source is designated as Cetacean morbillivirus
C:Superfamily: parainfluenza virus cell fusion protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-552/Product: fusion protein #status predicted <MAT>

Query Match 65.6%; Score 59; DB 2; Length 552;
Best Local Similarity 50.0%; Pred. No. 0.061;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
DB 289 TLSEVKGIVHRLAVSY 306

RESULT 8

VENZCD
cell fusion glycoprotein precursor - canine distemper virus
N:Contains: fusion protein F1; fusion protein F2
C:Species: canine distemper virus
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C:Accession: J50321
R:Barrett, T.; Clarke, D.K.; Evans, S.A.; Rima, B.K.
Virus Res. 8, 373-386, 1987
A:Title: The nucleotide sequence of the gene encoding the F protein of canine distemper
A:Reference number: J50321; M01D:88129050; PMID:3433924
A:Accession: J50321
A:Molecule type: mRNA
A:Residues: 1-662 <BAR>
A:Cross-references: GB:M21849; NID:G323241; PIDN:AAA42878.1; PID:G323242
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-135/Domain: signal sequence #status predicted <SIG>
F:136-224/Product: cell fusion glycoprotein F2 #status predicted <F2P>
F:225-662/Product: cell fusion glycoprotein F1 #status predicted <F1P>
F:606-629/Domain: transmembrane #status predicted <MEM>
F:62-141,173,179,517/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 65.6%; Score 59; DB 1; Length 662;
Best Local Similarity 50.0%; Pred. No. 0.074;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
DB 399 TLSEVKGIVHRLAVSY 416

RESULT 9

S21382
cell fusion protein - canine distemper virus
C:Species: canine distemper virus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S21382

R:Wild, T.F.; Bernard, A.; Spehner, D.; Villeval, D.; Drillean, R.
submitted to the EMBL Data Library, April 1992
A:Description: Vaccination of mice against canine distemper virus induced encephalitis
A:Reference number: S21382
A:Accession: S21382
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-662 <WTL>
A:Cross-references: EMBL:X65509; NID:G58853; PIDN:CAA46481.1; PID:G58854
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 65.6%; Score 59; DB 2; Length 662;
Best Local Similarity 50.0%; Pred. No. 0.074;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
DB 399 TLSEVKGIVHRLAVSY 416

RESULT 10

P00376
cell fusion glycoprotein - measles virus (strain TT) (fragment)
C:Species: measles virus
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C:Accession: P00376
R:Schulz, T.F.; Hoed, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A:Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A:Reference number: P00374; M01D:92300360; PMID:1607874
A:Molecule type: genomic RNA
A:Residues: 1-282 <SCH>
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion

Query Match 64.4%; Score 58; DB 2; Length 282;
Best Local Similarity 55.6%; Pred. No. 0.046;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
DB 19 TLSEIKGIVHRLAVSY 36

RESULT 11

P00388
cell fusion glycoprotein - measles virus (strain Schwarz vaccine) (fragment)
C:Species: measles virus
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C:Accession: P00388
R:Schulz, T.F.; Hoed, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A:Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A:Reference number: P00374; M01D:92300360; PMID:1607874
A:Molecule type: genomic RNA
A:Residues: 1-282 <SCH>
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion

Query Match 64.4%; Score 58; DB 2; Length 282;
Best Local Similarity 55.6%; Pred. No. 0.046;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
DB 19 TLSEIKGIVHRLAVSY 36

RESULT 12

cell fusion glycoprotein precursor - subacute sclerosing panencephalitis virus (strain XJ00274
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: subacute sclerosing panencephalitis virus, SSPEV
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
C:Accession: J00274
R:Kumase, K.; Haga, T.; Yoshikawa, Y.; Sato, T.A.; Yamamuchi, K.
Virus Genes 4, 173-181, 1990
A:Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defective
A:Reference number: J00274; MUID:90385702; PMID:1698327
A:Accession: J00274
A:Molecule type: mRNA
A:Residues: 1-534 <KOV>
A:Cross-references: EMBL:D10548; NID:g222256; PIDN:BA01405.1; PID:g222257
A>Note: The authors translated the codon GTA for residue 459 as Gly and GGG for residue
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
P:1-22/Domain: signal sequence #status predicted <Sig>
P:23-107/Product: cell fusion glycoprotein F2 #status predicted <FP2>
P:108-534/Product: cell fusion glycoprotein F1 #status predicted <FP1>
P:498-514/Domain: transmembrane #status predicted <TMN>
P:6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 58; DB 1; Length 534;

Best Local Similarity 55.6%; Pred. No. 0.088;

Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVIVHRIETLP 19

DB 287 TLTSEIKGVIVHRLGVSY 304

RESULT 13

E48556
cell fusion glycoprotein precursor - measles virus (strain A/K-C)
C:Species: measles virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: E48556
R:Mori, T.; Sasaki, K.; Hashimoto, H.; Makino, S.
Virus Genes 7, 67-81, 1993
A:Title: Molecular cloning and complete nucleotide sequence of genomic RNA of the A/K-C
A:Reference number: A48556; MUID:93227570; PMID:8470368
A:Accession: E48556
A:Molecule type: genomic RNA
A:Residues: 1-550 <MOR>
A:Cross-references: GB:S58435; NID:g299460; PIDN:AA826145.1; PID:g299465
A>Note: sequence extracted from NCBI backbone (NCBI:129264, NCBI:P.129272)
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
P:1-22/Domain: signal sequence #status predicted <Sig>
P:23-107/Product: cell fusion glycoprotein F2 #status predicted <FP2>
P:108-550/Product: cell fusion glycoprotein F1 #status predicted <FP1>
P:111-138/Region: hydrophobic
P:495-514/Domain: transmembrane #status predicted <TMN>
P:6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 58; DB 1; Length 550;

Best Local Similarity 55.6%; Pred. No. 0.09;

Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVIVHRIETLP 19

DB 287 TLTSEIKGVIVHRLGVSY 304

Query Match 64.4%; Score 58; DB 1; Length 550;

Best Local Similarity 55.6%; Pred. No. 0.09;

Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVIVHRIETLP 19

DB 287 TLTSEIKGVIVHRLGVSY 304

Query Match 64.4%; Score 58; DB 1; Length 550;

Best Local Similarity 55.6%; Pred. No. 0.09;

Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 14

VGNZMV

cell fusion glycoprotein precursor - measles virus

C:Species: measles virus

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000

C:Accession: A26962; A25616; P00380; P00384

R:Buckland, R.; Gerald, C.; Barker, R.; Wild, T.F.

U. Gen. Virol. 68, 1695-1703, 1987

A:Title: Fusion glycoprotein of measles virus: nucleotide sequence of the gene and comp

A:Reference number: A92794; MUID:87224816; PMID:3585281

A:Accession: A26962

A:Molecule type: mRNA

A:Residues: 1-553 <BUC>

A:Cross-references: GB:D00090; NID:g222061; PIDN:BA00056.1; PID:g222062

A:Experimental source: strain Halle

R:Richardson, C.; Hall, D.; Greer, P.; Hasel, K.; Berkovich, A.; Englund, G.; Bellini,

Virol. 155, 508-523, 1986

A:Title: The nucleotide sequence of the mRNA encoding the fusion protein of measles vir

A:Reference number: A94350; MUID:87071668; PMID:3788062

A:Accession: A25616

A:Molecule type: mRNA

A:Residues: 4-553 <RIC>

A:Cross-references: GB:M14915; NID:g331762; PIDN:AAA46423.1; PID:g331763

A:Experimental source: strain Edmonston

R:Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.

U. Gen. Virol. 73, 1581-1586, 1992

A:Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisc

A:Reference number: P00374; MUID:92300360; PMID:1607874

A:Accession: P00380

A:Molecule type: genomic RNA

A:Residues: 272-553 <SCH1>

A:Experimental source: isolate CL

A:Accession: P00384

A:Molecule type: genomic RNA

A:Residues: 272-553 <SCH2>

A:Experimental source: isolate SE

C:Genetics:

A:Gene: F

C:Superfamily: parainfluenza virus cell fusion protein

C:Keywords: glycoprotein; membrane fusion; transmembrane protein

P:1-25/Domain: signal sequence #status predicted <Sig>

P:26-110/Product: cell fusion glycoprotein F2 #status predicted <FP2>

P:111-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>

P:501-517/Domain: transmembrane #status predicted <TMN>

P:32,64,70/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 58; DB 1; Length 553;

Best Local Similarity 55.6%; Pred. No. 0.091;

Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVIVHRIETLP 19

DB 290 TLTSEIKGVIVHRLGVSY 307

RESULT 15

VGNZPD

cell fusion glycoprotein precursor - phocine distemper virus

N:Contains: fusion protein F1; fusion protein F2

C:Species: phocine distemper virus

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 25-Oct-1996

C:Accession: J01368

R:Koevamees, J.; Blixenkrone-Moeller, M.; Sharma, B.; Oerfell, C.; Norrby, E.

U. Gen. Virol. 72, 2959-2966, 1991

A:Title: The nucleotide sequence and deduced amino acid composition of the haemagglutin

A:Reference number: J01368; MUID:92113538; PMID:1765768

A:Accession: J01368

A:Molecule type: genomic RNA

A:Residues: 1-631 <KOV>

C:Genetics:

A:Gene: F

C:Superfamily: parainfluenza virus cell fusion protein

C:Keywords: glycoprotein; membrane fusion; transmembrane protein

P:1-188/Product: cell fusion glycoprotein F2 #status predicted <FP2>

P:89-106/Domain: transmembrane #status predicted <TM1>

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 3.73006 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-51
Perfect score: 90

Sequence: 1 ISITEIKGVHRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	71.1	546	1	VGIF_RINDL
2	61	67.8	546	1	VGIF_RINDR
3	60	66.7	546	1	VGIF_RINDR
4	59	65.6	662	1	VGIF_CDOV
5	58	64.4	534	1	VGIF_MEASV
6	58	64.4	550	1	VGIF_MEASA
7	58	64.4	550	1	VGIF_MEASB
8	58	64.4	631	1	VGIF_PHODV
9	54	60.0	546	1	VGIF_RINDK
10	50	55.6	529	1	VGIF_MEAS1
11	48	53.3	220	1	VGIF_MEAS1
12	48	53.3	229	1	VGIF_MEAS1
13	47	52.2	240	1	VGIF_MEAS1
14	44	48.9	219	1	VGIF_MEAS1
15	44	48.9	221	1	VGIF_MEAS1
16	42.5	47.2	529	1	VGIF_MEAS1
17	42.5	47.2	529	1	VGIF_MEAS1
18	42.5	47.2	529	1	VGIF_MEAS1
19	42.5	47.2	531	1	VGIF_MEAS1
20	41.5	46.1	392	1	VGIF_MEAS1
21	41	45.6	244	1	VGIF_MEAS1
22	41	45.6	244	1	VGIF_MEAS1
23	41	45.6	244	1	VGIF_MEAS1
24	41	45.6	1140	1	VGIF_MEAS1
25	40	44.4	127	1	VGIF_MEAS1
26	40	44.4	128	1	VGIF_MEAS1
27	40	44.4	235	1	VGIF_MEAS1
28	40	44.4	235	1	VGIF_MEAS1
29	40	44.4	565	1	VGIF_MEAS1
30	40	44.4	565	1	VGIF_MEAS1
31	40	44.4	565	1	VGIF_MEAS1
32	39	43.3	145	1	VGIF_MEAS1
33	39	43.3	204	1	VGIF_MEAS1

34	39	43.3	274	1	VGIF_HSV2
35	39	43.3	338	1	SYFA_FUSNM
36	39	43.3	365	1	GRAB_BACSV
37	39	43.3	381	1	ARGE_BUCAT
38	39	43.3	397	1	MPA2_AMEAR
39	39	43.3	701	1	TP20_YEAST
40	39	43.3	891	1	SECA_PAVLU
41	39	43.3	915	1	SYA_METKA
42	39	43.3	1704	1	VITI_FUNHE
43	38	42.2	141	1	PAZ2_ENTRA
44	38	42.2	198	1	PGD2_CHICK
45	38	42.2	208	1	PSD_METAC

ALIGNMENTS

RESULT 1	VGIF_RINDL	STANDARD;	PRT;	546 AA.
ID	VGIF_RINDL			
AC	P10864;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;			
DE	Fusion glycoprotein F1].			
GN	F.			
OS	Rinderpest virus (strain L) (RDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Paramyxovirinae; Morbillivirus.			
OX	NCBI_TaxID=11243;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88219541; PubMed=3285575;			
RA	Tsukiyama K., Yoshikawa Y., Yamanouchi K.;			
RT	Fusion glycoprotein (F) of rinderpest virus: entire nucleotide			
RT	sequence of the F mRNA, and several features of the F protein.;			
RL	Virology 164:523-530(1988).			
CC	-!- FUNCTION: This protein directs fusion of viral and cellular			
CC	membranes.			
CC	-!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2			
CC	LINKED BY A DISULFIDE BOND.			
CC	-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein			
CC	family.			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; M20870; AAA47399.1; -.			
DR	PIR; A28921; VGNZRL.			
DR	HSP; P04849; ISVF.			
DR	InterPro: IPR000776; Fusion gly.			
DR	Pfam; PF00523; fusion_gly; 1.			
KW	Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.			
FT	SIGNAL	1	19	
FT	CHAIN	20	546	
FT	CHAIN	20	108	
FT	CHAIN	109	546	
FT	DOMAIN	104	108	
FT	DOMAIN	109	123	
FT	TRANSMEM	484	513	
FT	TRANSMEM	514	517	
FT	DOMAIN	514	517	
FT	DOMAIN	514	517	
FT	DISULFID	64	191	
FT	CARBOHYD	25	57	
FT	CARBOHYD	57	57	
FT	CARBOHYD	63	63	
FT	SEQUENCE	546 AA;	58911 MW;	985029418728PFB5 CRC64;

Query Match 71.1%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.0028;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SITEIKGVIVRIETILP 19
Db 283 SLSEIKGVIVRIETILP 300

RESULT 2

VGLEF_RINDR STANDARD; PRT; 546 AA.

AC P41360;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain RPT1) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=39007;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95088609; PubMed=7996154;
RA Evans S.A., Baron M.D., Chamberlain R.W., Gootley L., Barrett T.;
RT "Nucleotide sequence comparisons of the fusion protein gene from
RT virulent and attenuated strains of rinderpest virus."
RL J. Gen. Virol. 75:3611-3617(1994).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.

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CC -----
DR EMBL; Z31656; CAA83482.1; -.
DR PIR; S47300; S47300.
DR HSSP; P04849; ISVP.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; Fusion gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 546
FT CHAIN 20 546
FT CHAIN 20 546
FT CHAIN 109 546
FT DOMAIN 104 108
FT TRANSMEM 109 133
FT TRANSMEM 484 513
FT DOMAIN 514 517
FT DISULFID 64 191
FT CARBOHYD 25 25
FT CARBOHYD 57 57
FT CARBOHYD 63 63
FT CARBOHYD 518 518
SQ SEQUENCE 546 AA; 58418 MW; 38853989344F401 CRC64;

Query Match 67.8%; Score 61; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.0093;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SITEIKGVIVRIETILP 19
Db 283 SLSEIKGVIVRIETILP 300

RESULT 3
VGLEF_RINDR STANDARD; PRT; 546 AA.

AC P41360;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain RBOX) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=39007;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95088609; PubMed=7996154;
RA Evans S.A., Baron M.D., Chamberlain R.W., Gootley L., Barrett T.;
RT "Nucleotide sequence comparisons of the fusion protein gene from
RT virulent and attenuated strains of rinderpest virus."
RL J. Gen. Virol. 75:3611-3617(1994).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.

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CC -----
DR EMBL; Z30700; CAA83186.1; -.
DR EMBL; Z30697; CAA83181.1; -.
DR PIR; S47305; S47305.
DR HSSP; P04849; ISVP.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; Fusion gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 546
FT CHAIN 20 546
FT CHAIN 20 546
FT CHAIN 109 546
FT DOMAIN 104 108
FT TRANSMEM 109 133
FT TRANSMEM 484 513
FT DOMAIN 514 517
FT DISULFID 64 191
FT CARBOHYD 25 25
FT CARBOHYD 57 57
FT CARBOHYD 63 63
FT CARBOHYD 518 518
SQ SEQUENCE 546 AA; 58705 MW; ED3DF8AFDBEBCB95 CRC64;

Query Match 66.7%; Score 60; DB 1; Length 546;
Best Local Similarity 55.6%; Pred. No. 0.014;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SITEIKGVIVRIETILP 19
Db 283 SLSEIKGVIVRIETILP 300

RESULT 4
VGLEF_CDVO STANDARD; PRT; 662 AA.
AC P12569; Q65991;

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01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DS Fusion glycoprotein F1].
GN F.
OS Canine distemper virus (strain Onderstepoort) (CDV) .
OC Viruses; ssRNA negative-strand viruses; Moroniogavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OC NCBI_TaxID=11233;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=88128050; PubMed=3433924;
RA Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
RT "The nucleotide sequence of the gene encoding the F protein of canine
RT distemper virus: a comparison of the deduced amino acid sequence with
RT other paramyxoviruses."
RL Vaccine 11:438-444(1993).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21849; AAA42878.1; -
DR EMBL: X65509; CAA46481.1; -
DR PIR: J50321; VGNZCD.
DR PIR: S21382; S21382.
DR HSSP: P04849; 1SVE.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; Fusion_gly; 1.
DR GlycoProtein: Fusion_protein; Transmembrane; Envelope protein; Signal.
DR SIGNAL 1 ? 662 FUSION GLYCOPROTEIN F0.
FT CHAIN 1 ? 662 PROTEIN F2.
FT CHAIN 2 224 PROTEIN F1.
FT TRANSMEM 606 629 POTENTIAL.
FT DISULFID 180 307 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 3 R -> K (IN REF. 2).
FT CONFLICT 140 140 D -> N (IN REF. 2).
FT CONFLICT 152 152 N -> S (IN REF. 2).
FT CONFLICT 171 171 I -> M (IN REF. 2).
FT CONFLICT 174 174 A -> V (IN REF. 2).
FT CONFLICT 662 662 L -> H (IN REF. 2).
SQ SEQUENCE 662 AA; 72970 MW; FRC81C9797805F0 CMC64;

Query Match 65.6%; Score 59; DB 1; Length 662;
Best Local Similarity 50.0%; Pred. NO. 0.025;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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DB	399	TLSEKGVIVHRLGAVS	416
RESULT 5			
VLGP_MEASA	STANDARD;	PRT;	534 AA.
ID	VLGP_MEASA		
AC	P26032;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-MAY-1992 (Rel. 22, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2; Fusion glycoprotein F1].		
GN	F.		
OS	Mesles virus (strain Yamagata-1) (Subacute sclerosing panencephalitis virus).		
OC	Viruses; ssRNA negative-strand viruses; Monomegavirales;		
OC	Paramyxoviridae; Paramyxovirinae; Morbilliviruses.		
OX	NCBI_TaxID=11239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=90385702; PubMed=1698327;		
RA	Komase K., Haga T., Yoshikawa Y., Sato T.A., Yamanouchi K.;		
RT	"Molecular analysis of structural protein genes of the Yamagata-1 strain of defective subacute sclerosing panencephalitis virus. IV.		
RT	Nucleotide sequence of the fusion gene.";		
RL	Virus Genes 4:173-181(1990).		
CC	-1- FUNCTION: This protein directs fusion of viral and cellular membranes.		
CC	-1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.		
CC	-1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.		
CC	-----		
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CC	-----		
DR	EMBL: D10548; BAA01405.1; -.		
DR	HSP: P04849; ISV.		
DR	InterPro: IPR000776; Fusion_gly.		
DR	Pfam: PF00523; fusion.gly; 1.		
KW	Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.		
FT	SIGNAL	1	23
FT	CHAIN	24	534
FT	CHAIN	24	112
FT	CHAIN	113	534
FT	TRANSMEM	113	136
FT	DOMAIN	137	494
FT	TRANSMEM	495	515
FT	DOMAIN	516	534
FT	DISULFID	68	195
FT	CARBOHYD	29	29
FT	CARBOHYD	61	61
FT	CARBOHYD	67	67
SO	SEQUENCE	534 AA;	57963 MM;
Query Match	64.4%;	Score 58;	DB 1;
Best Local Similarity	55.6%;	Pred. No. 0.03;	Length 534;
Matches 10;	Conservative 6;	Mismatches 2;	Indels 0;
0y	2	SITRKGVIVHRLGAVS	19
DB	287	TLSEKGVIVHRLGAVS	304
RESULT 6			
VLGP_MEASA	STANDARD;	PRT;	550 AA.
ID	VLGP_MEASA		
AC	P35973;		

DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DB Fusion glycoprotein F1].
 GN F.
 OS Measles virus (strain Aik-C) (Subacute sclerosing panencephalitis
 OS virus).
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 CC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 CC NCBI_TaxID=36408;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=93227570; PubMed=8470368;
 CC Mori T., Sasaki K., Hashimoto H., Makino S.;
 CC "Molecular cloning and complete nucleotide sequence of genomic RNA of
 CC the Aik-C strain of attenuated measles virus.";
 CC Virus Genes 7:67-81 (1993).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC -----
 CC EMBL: S58435; AAB26145.1; -
 CC PIR: E48556; E48556.
 CC DR HSSE; P04849; ISVF.
 CC DR InterPro: IPR000776; Fusion_gly.
 CC DR Pfam: PF00523; fusion_gly; 1
 CC KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 550 FUSION GLYCOPROTEIN F0.
 CC FT CHAIN 24 550 PROTEIN F2.
 CC FT CHAIN 113 550 PROTEIN F1.
 CC FT TRANSMEM 113 136 POTENTIAL.
 CC FT DOMAIN 137 494 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 495 515 POTENTIAL.
 CC FT DOMAIN 516 550 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 68 195 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 CC FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SO SEQUENCE 550 AA; 59540 MW; AACGADB92DE0D938 CRC64;
 CC
 CC Query Match 64.4%; Score 58; DB 1; Length 550;
 CC Best Local Similarity 55.6%; Pred. No. 0.03;
 CC Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC Oy 2 SITRKIVYRIETILP 19
 CC Db 287 TLSIKGVIVHRLGVSY 304
 CC
 CC RESULT 7
 CC VGLP_MEASR STANDARD; PRT; 550 AA.
 CC AC P08300;
 CC DT 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-AUG-1988 (Rel. 08, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DB Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 CC DB Fusion glycoprotein F1].
 CC GN F.
 CC OS Measles virus (strain Edmonston) (Subacute sclerosing panencephalitis

OS virus).
 OS Measles virus (strain Hallé) (Subacute sclerosing panencephalitis
 OS virus).
 OS Measles virus (strain Leningrad-16) (Subacute sclerosing panencephalitis
 OS virus).
 OS Measles virus (strain Edmonston-Zagreb) (Subacute sclerosing
 OS panencephalitis virus).
 OS Measles virus (strain Philadelphia-26) (Subacute sclerosing
 OS panencephalitis virus), and
 OS Measles virus (strain Edmonston B) (Subacute sclerosing panencephalitis
 OS virus).
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 CC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 CC NCBI_TaxID=11235, 11236, 70147, 70149, 70148, 70146;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Edmonston;
 CC MEDLINE=87224816; PubMed=3788062;
 CC Richardson C.D., Hull D., Greer P., Hasel K., Berkovich A.,
 CC Englund G., Bellini W.J., Rima B., Lazzarini R.A.;
 CC "The nucleotide sequence of the mRNA encoding the fusion protein of
 CC measles virus (Edmonston strain): a comparison of fusion proteins
 CC from several different paramyxoviruses.";
 CC Virology 155:508-523 (1986).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Hallé;
 CC MEDLINE=87224816; PubMed=3585281;
 CC Buckland R., Gerald C., Barker R., Wild T.F.;
 CC "Fusion glycoprotein of measles virus: nucleotide sequence of the
 CC gene and comparison with other paramyxoviruses.";
 CC J. Gen. Virol. 68:1695-1703 (1987).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Edmonston;
 CC MEDLINE=90085790; PubMed=2596022;
 CC Cattaneo R., Schmid A., Spielhofer P., Kaelin K., Bacsko K.,
 CC Meulen V., Pardowitz J., Planagan S., Rima B.K., Udem S.A.;
 CC "Mutated and hypermutated genes of persistent measles viruses which
 CC caused lethal human brain diseases.";
 CC Virology 173:415-425 (1989).
 CC [4]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Edmonston;
 CC MEDLINE=92263801; PubMed=1585658;
 CC Schmid A., Spielhofer P., Cattaneo R., Bacsko K., Ter Meulen V.,
 CC Billeter M.A.;
 CC "Subacute sclerosing panencephalitis is typically characterized by
 CC alterations in the fusion protein cytoplasmic domain of the
 CC persisting measles virus.";
 CC Virology 188:910-915 (1992).
 CC [5]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Edmonston, Leningrad-16, and Edmonston-Zagreb;
 CC MEDLINE=94249283; PubMed=8191786;
 CC Rota J.S., Wang Z.D., Rota P.A., Bellini W.J.;
 CC "Comparison of sequences of the H, F, and N coding genes of measles
 CC virus vaccine strains.";
 CC Virus Res. 31:317-330 (1994).
 CC [6]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Philadelphia-26;
 CC MEDLINE=94303181; PubMed=8030232;
 CC Hummel K.B., Vanchiere J.A., Bellini W.J.;
 CC "Restriction of fusion protein mRNA as a mechanism of measles virus
 CC persistence.";
 CC Virology 202:665-672 (1994).
 CC [7]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Edmonston B;
 CC Billeter M.A.;
 CC Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This protein directs fusion of viral and cellular

```

CC      membranes.
CC      -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC      LINKED BY A DISULFIDE BOND.
CC      -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC      family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL, M14915; AAA46423.1; -
CC      DR EMBL, X05597; AAA29090.1; ALT_INIT.
CC      DR EMBL, K01711; AAA75498.1; ALT_INIT.
CC      DR EMBL, K01711; AAA75499.1; -
CC      DR EMBL, U03659; AAA56647.1; ALT_INIT.
CC      DR EMBL, U03659; AAA56649.1; ALT_INIT.
CC      DR EMBL, U03670; AAA56650.1; ALT_INIT.
CC      DR EMBL, U08416; AAA50550.1; ALT_INIT.
CC      DR EMBL, Z66517; CAA91367.1; ALT_INIT.
CC      DR EMBL, Z66517; CAA91368.1; -
CC      DR HSSP, P04849; 1SVP.
CC      DR InterPro, IPR000776; Fusion_gly.
CC      DR Pfam, PF00523; Fusion_gly; 1.
CC      KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC      FT SIGNAL 1 23
CC      FT CHAIN 24 550 FUSION GLYCOPROTEIN F0.
CC      FT CHAIN 24 112 PROTEIN F2.
CC      FT CHAIN 113 550 PROTEIN F1.
CC      FT TRANSMEM 113 136 POTENTIAL.
CC      FT DOMAIN 137 494 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 495 515 POTENTIAL.
CC      FT DOMAIN 516 550 CYTOPLASMIC (POTENTIAL).
CC      FT DISULFID 68 195 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
CC      FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      SQ SEQUENCE 550 AA; 59532 MW; 7AA4F1CA82169093 CRC64;

Query Match 64.4%; Score 58; DB 1; Length 550;
Best Local Similarity 55.6%; Pred. No. 0.031; 2; Indels 0; Gaps 0;
Matches 10; Conservative 6; Mismatches 0;

QY 2 SITEIKGVIVHRIETILF 19
DB 287 TISEIKGVIVHRLKGVSY 304

RESULT 8
VGLF PHODV STANDARD; PRT; 631 AA.
AC P28886;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Nonnegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses;
OC NCBI_TaxID=11240;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate DK88-4A;
RC MEDLINE=92113538; PubMed=1765768;
RC Koevamees J., Blixenkron-Moeller M., Sharma B., Oerwell C.,
RC Norby B.;
DE "The nucleotide sequence and deduced amino acid composition of the
DE haemagglutinin and fusion proteins of the morbillivirus phocid

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RT distemper virus.";
RL J. Gen. Virol. 72:2959-2966(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Oister/88;
RC MEDLINE=92398437; PubMed=1524494;
RA Curran M.D., Lu Y.J., Rima B.K.;
RT "The fusion protein gene of phocine distemper virus: nucleotide and
RT deduced amino acid sequences and a comparison of morbillivirus fusion
RT proteins.";
RL Arch. Virol. 126:159-169(1992).
RN [3]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=Oister/88;
RC MEDLINE=91089508; PubMed=2264246;
RA Curran M.D., Loan D.O., Rima B.K., Kennedy S.;
RT "Nucleotide sequence analysis of phocine distemper virus reveals its
RT distinctness from canine distemper virus.";
RL Vet. Rec. 127:430-431(1990).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC -----
CC EMBL, D10371; BAA01206.1; -
CC DR PIR, A48346; A48346.
CC DR PIR, J01368; VGNZPD.
CC DR HSSP, P04849; 1SVP.
CC DR InterPro, IPR000776; Fusion_gly.
CC DR Pfam, PF00523; Fusion_gly; 1.
CC KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC FT SIGNAL 1 7
CC FT CHAIN 2 631 FUSION GLYCOPROTEIN F0.
CC FT CHAIN 2 188 F2 PROTEIN.
CC FT CHAIN 194 631 F1 PROTEIN.
CC FT DISULFID 149 276 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
CC FT TRANSMEM 89 106 POTENTIAL.
CC FT TRANSMEM 194 212 POTENTIAL.
CC FT TRANSMEM 575 595 POTENTIAL.
CC FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFICT 63 63 I -> V (IN REF. 2).
CC SQ SEQUENCE 631 AA; 68873 MW; D1FC87CDD426E9B8 CRC64;

Query Match 64.4%; Score 58; DB 1; Length 631;
Best Local Similarity 44.4%; Pred. No. 0.035; 2; Indels 0; Gaps 0;
Matches 8; Conservative 8; Mismatches 2;

QY 2 SITEIKGVIVHRIETILF 19
DB 368 TISEIKGVIVHRLKGVSY 385

RESULT 9
VGLF RINDK STANDARD; PRT; 546 AA.
AC P12574;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].

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GN F.
OS Rinderpest virus (strain Kabete O) (RNV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirinae.
OX NCBI_TaxID=11242;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=89322864; PubMed=3413983;
RA Hsu D., Yamashita M., Miller J., Dale B., Grubman M., Ylma T.;
RT "Cloning of the fusion gene of rinderpest virus: comparative sequence
RT analysis with other morbilliviruses."
RL Virology 166:149-153(1998).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M21514; AAA47400.1; -.
CC FIRM; A31051; VGNZK.
CC HSSP; P04849; ISVF.
CC InterPro: IPR000776; Fusion_gly.
CC Pfam; PF00523; fusion_gly; I.
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC SIGNAL
CC CHAIN 1 13
CC CHAIN 20 546
CC CHAIN 109 108
CC CHAIN 104 108
CC TRANSMEM 109 133
CC TRANSMEM 484 513
CC DOMAIN 514 517
CC DISULFID 64 191
CC CARBOHYD 25 25
CC CARBOHYD 57 57
CC CARBOHYD 63 63
CC CARBOHYD 518 518
CC SEQUENCE 546 AA; 58662 MW; 476D74DC18BCFCP CRC64;

Query Match 60.0%; Score 54; DB 1; Length 546;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 SITEIKGVIVRIETILF 19
DB 283 SLSEIKGVIVRIETILFVS 300
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RP SEQUENCE FROM N.A.
RX MEDLINE=92263801; PubMed=1585658;
RA Schmidt A., Spielhofer P., Cattaneo R., Bacsko K., Ter Meulen V.,
RA Billeter M.A.;
RT "Subacute sclerosing panencephalitis is typically characterized by
RT alterations in the fusion protein cytoplasmic domain of the
RT persisting measles virus."
RL Virology 188:910-915(1992).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16566; CAA34567.1; -.
CC EMBL; X16566; CAA34568.1; ALT_INIT.
CC HSSP; P04849; ISVF.
CC InterPro: IPR000776; Fusion_gly.
CC Pfam; PF00523; fusion_gly; I.
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC SIGNAL
CC CHAIN 1 26
CC CHAIN 27 529
CC CHAIN 27 115
CC CHAIN 116 529
CC TRANSMEM 116 139
CC TRANSMEM 140 497
CC DOMAIN 498 518
CC TRANSMEM 519 529
CC DOMAIN 529 529
CC DISULFID 71 198
CC CARBOHYD 32 32
CC CARBOHYD 64 64
CC CARBOHYD 70 70
CC SEQUENCE 529 AA; 57331 MW; AE987BC9F07E9A9A9 CRC64;

Query Match 55.6%; Score 50; DB 1; Length 529;
Best Local Similarity 50.0%; Pred. No. 0.72;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 SITEIKGVIVRIETILF 19
DB 290 TLSEIKGVIVRIETILFVS 307
:::|||||:::

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RESULT 10
VGLF MEASI STANDARD; PRT; 529 AA.
AC P26031; Q83298;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DB Fusion glycoprotein F1].
GN F.
OS Measles virus (strain IP-3-Ca) (Subacute sclerosing panencephalitis
OS virus).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirinae.
OX NCBI_TaxID=11237;
RN [1]

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RESULT 11
V725 ARATH STANDARD; PRT; 220 AA.
AC O48850;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Vesicle-associated membrane protein 725 (AtVAMP725).
GN VAMP725 OR AT2G32670 OR P24L7.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusteroideae; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.B., Feldblyum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

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RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nieman W.C., White O., Bisen J.A., Salzberg S.L., Frazer C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport vesicles to their target membrane (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
 CC -1- SIMILARITY: Contains 1 longin domain.
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 CC -----
 DR EMBL: AC003974; AAC04496.1; -
 DR PIR: T00801; T00801.
 DR InterPro: IPR001388; Synaptobrevin.
 DR Pfam: PF00957; synaptobrevin.1.
 DR PRINTS: PR00219; SYNAPTOBREVN.
 DR ProDom: PD001229; Synaptobrevin; 1.
 DR PROSITE: PS50859; LONGIN; 1.
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.
 DR PROSITE: PS50892; v-SNARE; 1.
 DR Transport; Protein transport; Transmembrane; Coiled coil;
 KW Multigene family.
 FT DOMAIN 1 196 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 197 217 ANCHOR FOR TYPE IV MEMBRANE PROTEIN (POTENTIAL).
 FT DOMAIN 218 220 VESICULAR (POTENTIAL).
 FT DOMAIN 10 114 LONGIN.
 FT DOMAIN 130 190 v-SNARE COILED-COIL HOMOLOGY.
 SQ SEQUENCE 220 AA; 24938 MW; F39F8FA03481DF5 CRC64;
 Query Match 53.3%; Score 48; DB 1; Length 220;
 Best Local Similarity 50.0%; Pred. No. 0.68; 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 3;
 QY 3 ITEIKGVIVHRIETIL 18
 Db 138 VTEVKGVMENIEKVL 153
 RESULT 12
 ID V726 ARATH STANDARD; PRT; 229 AA.
 AC 09MAY55;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Putative vesicle-associated membrane protein 726 (AtVAMP726).
 GN VAMP726 OR AT1G04760 OR F13M7.25.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Becker U.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooke S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen X., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Begu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.E., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marzilli A.,
 RA Miltchev J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.R., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utechtack T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis thaliana*.";
 RL Nature 408:816-820(2000).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport vesicles to their target membrane (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
 CC -1- SIMILARITY: Contains 1 longin domain.
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 CC -----
 DR EMBL: AC004809; AAF0460.1; -
 DR PIR: F86180; F86180.
 DR InterPro: IPR001388; Synaptobrevin.
 DR Pfam: PF00957; synaptobrevin.1.
 DR PRINTS: PR00219; SYNAPTOBREVN.
 DR ProDom: PD001229; Synaptobrevin; 1.
 DR PROSITE: PS50859; LONGIN; 1.
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.
 DR PROSITE: PS50892; v-SNARE; 1.
 DR Hypothetical protein; Transport; Protein transport; Transmembrane;
 KW Coiled coil; Multigene family.
 FT DOMAIN 1 205 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 206 226 ANCHOR FOR TYPE IV MEMBRANE PROTEIN (POTENTIAL).
 FT DOMAIN 227 229 VESICULAR (POTENTIAL).
 FT DOMAIN 10 114 LONGIN.
 FT DOMAIN 130 199 v-SNARE COILED-COIL HOMOLOGY.
 SQ SEQUENCE 229 AA; 25867 MW; B4217AB7EF419E35 CRC64;
 Query Match 53.3%; Score 48; DB 1; Length 229;
 Best Local Similarity 50.0%; Pred. No. 0.71; 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 3;
 QY 3 ITEIKGVIVHRIETIL 18
 Db 138 VTEVKGVMENIEKVL 153
 RESULT 13
 ID V727 ARATH STANDARD; PRT; 240 AA.
 AC 09MAY55;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Vesicle-associated membrane protein 727 (AtVAMP727).
 GN VAMP727 OR AT3G54300 OR F24B2.260.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansgore W., Unsel M.,
 RA Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaler B.,
 RA Delaney M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Cholice N., Artiguenave F., Robert C., Brothier P.,
 RA Wincker P., Catcollo L., Weisenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Muller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordlek G.,
 RA Reichelt J., Scharte C., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemant D.,
 RA Cooke R., Landie M., Berger-Laurio C., Purnelle B., Masuy D.,
 RA de Haan M., Maestre A.C., Alcaraz J.-P., Cotter A., Casachubeta E.,
 RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Malet R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltcher J., Sellers P., Gill J.B., Feldlyum T.V.,
 RA Preuss D., Lin X., Niemman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Aamitsu E.,
 RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shippo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana."
 RL Nature 408:820-822(2000).
 CC -!- FUNCTION: Involved in the targeting and/or fusion of transport
 CC vesicles to their target membrane (by similarity).
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the synaptobrevin family.
 CC -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
 CC -!- SIMILARITY: Contains 1 longin domain.
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 CC -----
 CC EMBL, AL132957; CAB71004.1; -
 DR PIR, T47589; T47589.
 DR InterPro, IPR001388; Synaptobrevin.
 DR Pfam, PF00957; synaptobrevin; 1.
 DR PRINTS, PR00219; SYNAPTOBREVIN.
 DR PRODOM, PD001229; Synaptobrevin; 1.
 DR PROSITE, PS50859; LONGIN; 1.
 DR PROSITE, PS50417; SYNAPTOBREVIN; 1.
 DR PROSITE, PS50892; V-SNARE; 1.
 KM Transport; Protein transport; Transmembrane; Coiled coil;
 KM Multigene family.
 FT DOMAIN 1 215 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 216 236 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 FT (POTENTIAL).
 FT DOMAIN 237 240 VESICULAR (POTENTIAL).
 FT DOMAIN 6 133 LONGIN.
 FT DOMAIN 149 209 V-SNARE COILED-COIL HOMOLOG.
 RT SEQUENCE 240 AA; 27459 MW; 4805B9406B95D47B CRC64;
 QO Query Match 52.2%; Score 47; DB 1; Length 240;
 Best Local Similarity 50.0%; Pred. No. 1.1;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 3 IITKGVVHRIETIL 18
 DB 157 IITVIGIMQNIKIVL 172

RESULT 14
 ID V721 ARATH STANDARD; PRT; 219 AA.
 AC Q92TW3; O23011; Q9MAS4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Vesicle-associated membrane protein 721 (AtVAMP721) (v-SNARE
 DE synaptobrevin 721) (AtVAMP721).
 GN VAMP721 OR VAMP7B OR AT1G04740/AT1G04750 OR TIG11.1 OR F13M7_23 OR
 GN F13M7_26.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OC NCBI_TaxId=3702;
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Becker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Alatafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.P., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 RA Dunn P., Egu J., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Marshall A.,
 RA Malt G., Peterson J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pail G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shim P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Tortini M.J., Town C.D.,
 RA Uteback T., Van Aken S., Vayberg M., Vyeotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana."
 RL Nature 408:816-820(2000).
 (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp W., Chang C.H., Lee J.M., Tortini M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anzari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Egu J., Goldsmith A.D., Gurli M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tanabe R., Vayberg M., Wallender B.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Becker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome."
 RL Science 302:842-846(2003).
 CC -!- FUNCTION: Involved in the targeting and/or fusion of transport
 CC vesicles to their target membrane (by similarity).
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (by similarity).
 CC -!- SIMILARITY: Belongs to the synaptobrevin family.
 CC -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
 CC -!- SIMILARITY: Contains 1 longin domain.
 CC -!- CAUTION: Ref.2 sequences differ from that shown due to erroneous
 CC gene model prediction.

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CC -----

DR EMBL; AC025333; AAC98905.1; -
 DR EMBL; AC002376; AAB80624.1; ALT_SEQ.
 DR EMBL; AC004809; AAF40468.1; ALT_SEQ.
 DR EMBL; AY079164; AAL85003.1; -
 DR EMBL; AY133661; AAM91491.1; -
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam: PF00957; synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS50859; LONGIN; 1.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS50892; V_SNARE; 1.
 DR Transport; Protein transport; Transmembrane; Coiled coil;
 DR Multigene family.
 DR TRANSMEM 1 196 CYTOPLASMIC (POTENTIAL).
 DR DOMAIN 197 217 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 DR DOMAIN 218 219 (POTENTIAL).
 DR DOMAIN 10 114 VESICULAR (POTENTIAL).
 DR DOMAIN 130 190 LONGIN.
 DR SEQUENCE 219 AA; 24765 MW; 7F234FDB5138082 CRC64;

Query Match 48.9%; Score 44; DB 1; Length 219;
 Best Local Similarity 43.8%; Pred. No. 3.3;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ITKIKGVIVRIETIL 18
 Db 138 VSEVKGVMMENIKVL 153

RESULT 15
 V722 ARATH STANDARD; PRT; 221 AA.
 AC P47152; 049321;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Vesicle-associated membrane protein 722 (AtVAMP722) (Synaptoobrevin-
 DE related protein 1)
 GN VAMP722 OR SARI OR HAT24 OR AT2G33120 OR P25118.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Burkholderia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.B., Feldblyum T.V.,
 RA Beell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Kuo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Bisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brever V., Trouhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Phan P.K., Chouk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome";
 RL Science 302:842-846(2003).
 RN [5]
 RP SEQUENCE OF 140-200 FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=9223725; PubMed=1349174;
 RA Schena M., Davis R.W.;
 RT "HD-Zip proteins: members of an Arabidopsis homeodomain protein
 RT superfamily";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3894-3898(1992).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
 CC vesicles to their target membrane (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the synaptoobrevin family.
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
 CC -1- SIMILARITY: Contains 1 longin domain.

CC -----

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DR EMBL; M90418; AAB56991.1; -
 DR EMBL; AC002334; AAC04921.1; -
 DR EMBL; AY086363; AAM64431.1; -
 DR EMBL; AY072422; AAL62414.1; -
 DR EMBL; AP419564; AAL31896.1; -
 DR EMBL; AY079037; AAL79387.1; -
 DR EMBL; AY114706; AAM48025.1; -
 DR EMBL; AY128288; AAM91096.1; -
 DR PIR; F84741; F84741.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam: PF00957; synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS50859; LONGIN; 1.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS50892; V_SNARE; 1.
 DR Transport; Protein transport; Transmembrane; Coiled coil;
 DR Multigene family.
 DR DOMAIN 1 196 CYTOPLASMIC (POTENTIAL).
 DR TRANSMEM 197 217 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 DR (POTENTIAL).

FT	DOMAIN	218	221	VESICULAR (POTENTIAL).
FT	DOMAIN	10	114	LONGIN.
FT	DOMAIN	130	190	V-SNARE COILED-COIL HOMOLOG.
FT	CONFLICT	123	123	D -> A (IN REF. 1).
SO	SEQUENCE	221 AA;	24928 MM;	880AA/BA2C24697B CRC64;

Query Match 48.9%; Score 44; DB 1; Length 221;
 Best Local Similarity 43.8%; Pred. No. 3.4;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY	3	ITBIKGVIVHRIETIL	18
	::: :: :: ::		
Db	138	VSEYKGVMMENIRKYL	153

Search completed: June 18, 2004, 19:59:36
 Job time : 4.73006 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: June 18, 2004, 19:53:15 ; Search time 18.4172 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-51

Perfect score: 90

Sequence: 1 ISITRIKGVYVRIETILF 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

SPTREMBL_25:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	61	67.8	546	12 Q91HA5	Q91HA5 rinderpest
2	60	66.7	546	12 Q84926	Q84926 peste-des-p
3	59	65.6	528	12 Q9YJW9	Q9YJW9 canine dist
4	59	65.6	530	12 Q8OV06	Q8OV06 canine dist
5	59	65.6	552	12 Q66147	Q66147 cetacean mo
6	59	65.6	662	12 Q9DX22	Q9DX22 canine dist
7	59	65.6	662	12 Q91KN3	Q91KN3 canine dist
8	59	65.6	662	12 Q9YKL7	Q9YKL7 canine dist
9	59	65.6	662	12 Q89327	Q89327 canine dist
10	58	64.4	534	12 Q04243	Q04243 measles vir
11	58	64.4	537	12 Q04242	Q04242 measles vir
12	58	64.4	545	12 Q9PXA4	Q9PXA4 measles vir
13	58	64.4	550	12 P90331	P90331 measles vir
14	58	64.4	550	12 Q9QBX0	Q9QBX0 measles vir
15	58	64.4	550	12 Q9QBW9	Q9QBW9 measles vir
16	58	64.4	550	12 P90330	P90330 measles vir

17	58	64.4	550	12 Q9QEW7	Q9QEW7 measles vir
18	58	64.4	550	12 Q9WVK4	Q9WVK4 measles vir
19	58	64.4	550	12 Q89495	Q89495 measles vir
20	58	64.4	550	12 Q8V049	Q8V049 measles vir
21	58	64.4	550	12 Q9Y094	Q9Y094 measles vir
22	58	64.4	550	12 Q9QEX1	Q9QEX1 measles vir
23	58	64.4	550	12 Q9QEW8	Q9QEW8 measles vir
24	58	64.4	553	12 Q93055	Q93055 measles vir
25	58	64.4	553	12 Q9IC36	Q9IC36 measles vir
26	58	64.4	553	12 P88973	P88973 measles vir
27	58	64.4	553	12 Q83536	Q83536 measles vir
28	58	64.4	553	12 Q11383	Q11383 measles vir
29	58	64.4	553	12 Q91FK2	Q91FK2 measles vir
30	58	64.4	553	12 Q83533	Q83533 measles vir
31	58	64.4	553	12 Q83525	Q83525 measles vir
32	58	64.4	553	12 Q83518	Q83518 measles vir
33	58	64.4	553	12 P88974	P88974 measles vir
34	58	64.4	553	12 Q83527	Q83527 measles vir
35	58	64.4	553	12 Q83521	Q83521 measles vir
36	58	64.4	553	12 Q83530	Q83530 measles vir
37	58	64.4	553	12 Q91248	Q91248 measles vir
38	58	64.4	553	12 Q910P2	Q910P2 measles vir
39	58	64.4	553	12 Q04244	Q04244 measles vir
40	58	64.4	579	12 Q9PWT4	Q9PWT4 measles vir
41	56	62.2	552	12 Q66409	Q66409 dolphin mor
42	56	62.2	552	12 Q56852	Q56852 dolphin mor
43	56	62.2	553	12 Q11380	Q11380 measles vir
44	54	60.0	545	12 Q9QEW6	Q9QEW6 measles vir
45	48	53.3	285	10 Q8GXC1	Q8GXC1 arabidopsis

ALIGNMENTS

RESULT 1

Q91HA5 ID Q91HA5 PRELIMINARY; PRT; 546 AA.
AC Q91HA5;
DT 01-DEC-2001 (TREMURel. 19, Created)
DT 01-DEC-2001 (TREMURel. 19, Last sequence update)
DT 01-OCT-2003 (TREMURel. 25, Last annotation update)
DE Fusion protein.
OS F.
GN Rinderpest virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RX MEDLINE=21014265; PubMed=11186456;
RA Alano P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V., Gusev A.A.;
RT "Primary structure of the F-gene from Rinderpest virus strain K.";
RL Mol. Gen. Microbiol. Virol. 4:29-33(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RA Ayano P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V., Gusev A.A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY035887; AAK63190.1; -;
DR PIR: P00866; P00866.
DR PIR: P00867; P00867.
DR PIR: P00873; P00873.
DR GO: GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO: GO:006948; F:Viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; I.
SQ SEQUENCE 546 AA; 58572 MW; 44982BD7405F0B CRC64;
Query Match 67.8%; Score 61; DB 12; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.094;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVVHRIETLP 19
:::|||||:::
Db 283 SLSEIKGVVHRLKGVSY 300

RESULT 2
Q84926 PRELIMINARY; PRT; 546 AA.
AC Q84926;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Fusion protein.
GN F.
OS peste-des-petits-ruminants virus (PPRV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_Taxid=31604;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE STRAIN;
RX MEDLINE=96082318; PubMed=7483819;
RA Meyer G., Diallo A.;
RT "The nucleotide sequence of fusion protein gene of the peste des
petits ruminants virus: the long untranslated region in the 5' end of
the P gene of morbilliviruses seems to be specific to each virus.";
RL Virus Res. 37:23-35(1995).
DR EMBL; 237017; CA85451.1; -
DR PIR; S55386; S55386.
DR HSSP; P04849; 1SVF.
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR00776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 546 AA; 59310 MW; DPTD903A048A0BB CRC64;

Query Match 66.7%; Score 60; DB 12; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.14;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVVHRIETLP 19
:::|||||:::
Db 283 SLSEIKGVVHRLKGVSY 300

RESULT 3
Q9YJW9 PRELIMINARY; PRT; 528 AA.
AC Q9YJW9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Fusion protein precursor (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_Taxid=11232;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=2544/Han95; and CV. 5th passage Vero;
RA Liemann H., Harder T.C., Loeschelt M., Baumgaertner W., Moennig V.,
Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
proximal coding part of the P gene of wild-type and vaccine canine
distemper morbilliviruses.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=2544/Han95; and CV. 5th passage Vero;
RA Harder T.C., von Messling V., Oerwell C., Moennig V., Haas L.;

RT "Wild-type canine distemper virus nucleocapsid, fusion and
RT hemagglutinin protein expression in recombinant baculovirus.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ007711; CA07617.1; -
DR HSSP; P04849; 1SVF.
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR00776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
GN Signal.
FT NON_TER 1 1
FT SIGNAL <1 10 POTENTIAL.
FT CHAIN 11 >528 FUSION PROTEIN.
FT NON_TER 528 528
SQ SEQUENCE 528 AA; 57613 MW; 146C8CBF68F6516 CRC64;

Query Match 65.6%; Score 59; DB 12; Length 528;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVVHRIETLP 19
:::|||||:::
Db 272 TLSEVKGIVHRLKGVSY 289

RESULT 4
Q8QV06 PRELIMINARY; PRT; 530 AA.
AC Q8QV06;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_Taxid=11232;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=DOG/DK 91C;
RA Andersen M.K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF55188; AL83966.1; -
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR00776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
FT NON_TER 1 1
SQ SEQUENCE 530 AA; 57985 MW; 8F7173C247AF233D CRC64;

Query Match 65.6%; Score 59; DB 12; Length 530;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGVVHRIETLP 19
:::|||||:::
Db 267 TLSEVKGIVHRLKGVSY 284

RESULT 5
Q66147 PRELIMINARY; PRT; 552 AA.
AC Q66147;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Fusion protein precursor.
OS Cetacean morbillivirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_Taxid=36410;
RN (1)

RP SEQUENCE FROM N.A.
RC STRAIN=porpoise;
RX MEDLINE=95159670; PubMed=7531923;
RA Bole G.G.B., Blixenkroner-Moeller M.M.B., Gottschalk E., Wishaup R.G.,
RA Welsh M.J., Barle J.A.P., Rima B.K.;
RT "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT porpoise and a dolphin."
RU Virus Res. 34:291-304(1994).
DR EMBL: X80757; CAA56731.1; -.
DR PIR: S47034; S47034.
DR HSSP: P04849; 1SVF.
DR GO: GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; I.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 552 AA; 60025 MW; 40D919AD910EA1E CRC64;
POTENTIAL.
Query Match 1 25
Best Local Similarity 50.0%; Score 59; DB 12; Length 552;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SITEINGVIVHRIETILF 19
Db 289 TLSEVGVIVHRLAVSY 306

RESULT 6
Q9DXZ2 PRELIMINARY; PRT; 662 AA.
Q9DXZ2:

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein F.
OS Canine distemper virus (strain Onderstepoort) (CDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11233;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Onderstepoort;
RX MEDLINE=20499096; PubMed=11044118;
RA Gassem U., Collins F.M., Duprex W.P., Rima B.K.;
RT "Establishment of a rescue system for canine distemper virus.";
RU J. Virol. 74:10737-10744(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Onderstepoort;
RA Gassem U., Collins F.M., Duprex P., Rima B.K.;
RU Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305419; AAC30919.1; -.
DR HSSP: P04849; 1SVF.
DR GO: GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; I.
SQ SEQUENCE 662 AA; 72988 MW; 9C5C1398C8AE7B4C CRC64;

Query Match 50.6%; Score 59; DB 12; Length 662;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SITEINGVIVHRIETILF 19
Db 399 TLSEVGVIVHRLAVSY 416

RESULT 7
Q91KN3 PRELIMINARY; PRT; 662 AA.
ID Q91KN3

AC Q91KN3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21306344; PubMed=11413309;
RA von Messling V., Zimmer G., Herrler G., Haas L., Cattaneo R.;
RT "The hemagglutinin of canine distemper virus determines tropism and
RT cytopathogenicity."
RU J. Virol. 75:6418-6427(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA von Messling V.A., Zimmer G., Herrler G., Haas L., Cattaneo R.;
RU Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF378705; AAK54668.1; -.
DR GO: GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; I.
SQ SEQUENCE 662 AA; 72898 MW; CC6A104A96B8F8A0 CRC64;

Query Match 65.6%; Score 59; DB 12; Length 662;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SITEINGVIVHRIETILF 19
Db 399 TLSEVGVIVHRLAVSY 416

RESULT 8
Q9YKL7 PRELIMINARY; PRT; 662 AA.
Q9YKL7:

DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A75/17;
RX MEDLINE=99139009; PubMed=9971809;
RA Cherpillod P., Beck K., Zurbriggen A., Wittek R.;
RT "Sequence analysis and expression of the attachment and fusion
RT proteins of canine distemper virus wild-type strain A75/17.";
RU J. Virol. 73:2263-2269(1999).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=A75/17;
RA Wiederkent C., Howley P., Zurbriggen A., Wittek R.;
RT "Complete sequence of canine distemper wildtype strain A75/17.";
RU Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF112188; AAD18007.1; -.
DR EMBL: AF164967; AAD49702.1; -.
DR HSSP: P04849; 1SVF.
DR GO: GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; I.
SQ SEQUENCE 662 AA; 72537 MW; 68F992DCBA51F0BA CRC64;

Query Match 65.6%; Score 59; DB 12; Length 662;

Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 SITEIKGIVHRIETILF 19
:::|||||:::|

Db 399 TLSBKGVVHRLBVS 416

RESULT 9

089327 PRELIMINARY; PRT; 662 AA.

AC 089327;
DT 01-NOV-1998 (TRMBLrel. 08, Created)

DT 01-NOV-1998 (TRMBLrel. 08, Last sequence update)

DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)

OS Canine distemper virus.
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.

NCBI_TaxID=11232;

SEQUENCE FROM N.A.

STRAIN=Onderstepoort;

RA Sidhu M.S., Husar W., Cook S.D., Dowling P.C., Udem S.A.;
"Canine distemper terminal and intergenic non-protein coding
nucleotide sequences: completion of the entire CDV genome sequence.";
Virology 193:66-72(1993).

SEQUENCE FROM N.A.

STRAIN=Onderstepoort;

RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR HSP; P04849; ISVF.

DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

DR InterPro; IPR000776; Fusion_gly.

DR Pfam; PF00523; fusion_gly; I.

DR SEQUENCE 662 AA; 72951 MW; 80B144C6B9801898 CRC64;

QY 2 SITEIKGIVHRIETILF 19
:::|||||:::|

Db 399 TLSBKGVVHRLBVS 416

RESULT 10

004243 PRELIMINARY; PRT; 534 AA.

AC 004243;
DT 01-NOV-1996 (TRMBLrel. 01, Created)

DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)

OS Measles virus.
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.

NCBI_TaxID=11234;

SEQUENCE FROM N.A.

STRAIN=89003063; PubMed=3167982;
Cattaneo R., Schmidt A., Eschle D., Baczko K., ter Meulen V.,
Billeter M.A.;
"Biased hypermutation and other genetic changes in defective measles
viruses in human brain infections.";
Cell 55:255-265(1988).

RT Cell 55:255-265(1988).

SEQUENCE FROM N.A.

RA Cattaneo R., Billeter M.A.;
RL Virology 0:0-0(0).

DR EMBL; X16568; CA34581.1; -.

DR EMBL; X16568; CA34582.1; -.

DR HSP; P04849; ISVF.

DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

DR InterPro; IPR000776; Fusion_gly.

DR Pfam; PF00523; fusion_gly; I.

DR SEQUENCE 534 AA; 57899 MW; 637245E23B5B044 CRC64;

RESULT 11

004242 PRELIMINARY; PRT; 537 AA.

AC 004242;
DT 01-NOV-1996 (TRMBLrel. 01, Created)

DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)

OS Measles virus.
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.

NCBI_TaxID=11234;

SEQUENCE FROM N.A.

STRAIN=89003063; PubMed=3167982;
Cattaneo R., Schmidt A., Eschle D., Baczko K., ter Meulen V.,
Billeter M.A.;
"Biased hypermutation and other genetic changes in defective measles
viruses in human brain infections.";
Cell 55:255-265(1988).

RT Cell 55:255-265(1988).

SEQUENCE FROM N.A.

STRAIN=Cattaneo R., Billeter M.A.;

VLirology 0:0-0(0).

DR EMBL; X16567; CA34574.1; -.

DR HSP; P04849; ISVF.

DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.

DR InterPro; IPR000776; Fusion_gly.

DR Pfam; PF00523; fusion_gly; I.

DR SEQUENCE 537 AA; 58275 MW; D0A60AC6D979E06 CRC64;

QY 2 SITEIKGIVHRIETILF 19
:::|||||:::|

Db 290 TLSBKGVVHRLBVS 307

RESULT 12

004243 PRELIMINARY; PRT; 545 AA.

AC 004243;
DT 01-MAY-2000 (TRMBLrel. 13, Created)

DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)

OS Measles virus.
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.

OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11234;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=OSA-3;
 RA Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;
 RT "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF179439; AAF02705.1; -;
 DR EMBL: AF179439; AAF02704.1; -;
 DR HSSP: P04849; ISVP.
 DR GO: GO:0019039; F:Viral-cell fusion molecule activity; IEA.
 DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro: IPR000776; Fusion_gly.
 DR Pfam: PF00523; fusion_gly; 1.
 SO SEQUENCE 545 AA; 58907 MW; 0234C28AB193E77D CRC64;
 Query Match 64.4%; Score 58; DB 12; Length 545;
 Best Local Similarity 55.6%; Pred. No. 0.31;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 2 SITEIKGVIVHRIETTLF 19
 DB 287 TLSEIKGVIVHRIEGVSY 304
 P00331 PRELIMINARY; PRT; 550 AA.
 AC P00331;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fusion protein.
 OS Measles virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11234;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NAGAHATA;
 RA Sheng J., Watanabe M., Ueda S.;
 RT "Selection of a neurotropic variant of measles virus.";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NAGAHATA;
 RA Sheng J., Nakaniishi M., Watanabe M., Ueda S.;
 RT "An amino acid alteration of F protein responsible for the enhanced fusogenicity of measles virus.";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NAGAHATA;
 RA Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;
 RT "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D63926; BA00958.1; -;
 DR EMBL: AF179431; AAF02696.1; -;
 DR PIR: P00376; P00376.
 DR HSSP: P04849; ISVP.
 DR GO: GO:0019039; F:Viral-cell fusion molecule activity; IEA.
 DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro: IPR000776; Fusion_gly.

DR Pfam: PF00523; fusion_gly; 1.
 SO SEQUENCE 550 AA; 59530 MW; 97C991C7B2169839 CRC64;
 Query Match 64.4%; Score 58; DB 12; Length 550;
 Best Local Similarity 55.6%; Pred. No. 0.31;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 2 SITEIKGVIVHRIETTLF 19
 DB 287 TLSEIKGVIVHRIEGVSY 304
 P00331 PRELIMINARY; PRT; 550 AA.
 AC P00331;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fusion protein.
 OS Measles virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11234;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOYOSHIMA;
 RA Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;
 RT "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF179432; AAF02697.1; -;
 DR PIR: P00376; P00376.
 DR HSSP: P04849; ISVP.
 DR GO: GO:0019039; F:Viral-cell fusion molecule activity; IEA.
 DR GO: GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro: IPR000776; Fusion_gly.
 DR Pfam: PF00523; fusion_gly; 1.
 SO SEQUENCE 550 AA; 59504 MW; 2AA969D37FA5CA17 CRC64;
 Query Match 64.4%; Score 58; DB 12; Length 550;
 Best Local Similarity 55.6%; Pred. No. 0.31;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 2 SITEIKGVIVHRIETTLF 19
 DB 287 TLSEIKGVIVHRIEGVSY 304
 P00331 PRELIMINARY; PRT; 550 AA.
 AC P00331;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fusion protein.
 OS Measles virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11234;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=OSA-2;
 RA Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;
 RT "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed.";

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 43.2515 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-71

Perfect score: 152
Sequence: 1 DABPRDGGYKISTIKGVYHRTILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	152	100.0	30 6	AAE35677 Human Abe
2	141	92.8	32 6	AAE35678 Human Abe
3	140	92.1	34 6	AAE35679 Human Abe
4	133	87.5	48 6	AAE35680 Human Abe
5	126	82.9	34 6	AAE35681 Human Abe
6	119	78.3	34 6	AAE35682 Human Abe
7	90	59.2	19 6	AAE35657 Measles v
8	90	59.2	31 7	ADD89946 CD4 pep1
9	90	59.2	45 7	ADD89951 IGR pep1
10	90	59.2	50 7	ADD89944 CD4 pep1
11	87	57.2	65 7	ADD89953 Foot-and-
12	83	54.6	65 7	ADD89952 Foot-and-
13	80.5	53.0	31 3	AAE35657 Measles v
14	78	51.3	29 3	AAE35657 Measles v
15	76	50.0	19 3	AAE35657 Measles v
16	76	50.0	19 3	AAE35657 Measles v
17	76	50.0	19 3	AAE35657 Measles v
18	76	50.0	19 3	AAE35657 Measles v
19	76	50.0	19 3	AAE35657 Measles v
20	76	50.0	19 3	AAE35657 Measles v
21	76	50.0	19 3	AAE35657 Measles v
22	76	50.0	29 3	AAE35657 Measles v
23	76	50.0	29 3	AAE35657 Measles v
24	76	50.0	29 3	AAE35657 Measles v
25	76	50.0	30 3	AAE35657 Measles v

26	76	50.0	30 5	ABG68233 Optimised
27	76	50.0	31 3	AAE35677 standard; peptide; 30 AA.
28	76	50.0	31 3	AAE35677 standard; peptide; 30 AA.
29	76	50.0	32 5	ABG68235 Optimised
30	76	50.0	34 5	ABG68231 Optimised
31	76	50.0	35 3	AAE35657 Measles v
32	76	50.0	36 3	AAE35657 Measles v
33	76	50.0	36 3	AAE35657 Measles v
34	76	50.0	36 3	AAE35657 Measles v
35	76	50.0	39 5	ABG68237 Optimised
36	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
37	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
38	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
39	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
40	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
41	76	50.0	46 3	AAE35677 standard; peptide; 30 AA.
42	76	50.0	47 3	AAE35677 standard; peptide; 30 AA.
43	76	50.0	47 3	AAE35677 standard; peptide; 30 AA.
44	76	50.0	49 3	AAE35677 standard; peptide; 30 AA.
45	76	50.0	51 3	AAE35677 standard; peptide; 30 AA.

ALIGNMENTS

RESULT 1	ID	AAE35677	standard; peptide; 30 AA.
AC	AAE35677		
DT	23-OCT-2003	(revised)	
DT	17-JUN-2003	(first entry)	
XX			
DE	Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.		
XX			
KW	Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;		
KW	Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;		
XX	vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.		
XX			
OS	Homo sapiens.		
OS	Measles virus.		
XX			
CH	Chimeric.		
FT	Key	Location/Qualifiers	
FT	Region	1..10	
FT	Region	14..30	
FT	Region	/note= "Measles virus T helper cell epitope"	
XX			
PN	WO200296350-A2.		
XX			
PD	05-DEC-2002.		
XX			
PF	02-APR-2002; 2002WO-US010293.		
XX			
PR	25-MAY-2001; 2001US-00865294.		
XX			
PI	(UNB1) UNITED BIOMEDICAL INC.		
XX			
DR	WPI; 2003-201258/19.		
XX			
PT	Novel peptide immunogen comprising a helper T cell epitope, an N-terminal		
PT	fragment of amyloid beta peptide linked to the epitope, and optionally a		
PT	spacer, useful for preventing or treating Alzheimer's disease.		
XX			
PS	Claim 9; Page 39; 77pp; English.		
XX			
CC	The present invention relates to a novel peptide immunogen comprising a		
CC	helper T cell (Th) epitope, an N-terminal fragment of amyloid beta		
CC	(Abeta) peptide (residues 1-42) linked to the epitope and optionally a		

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 30 AA;

Query Match 100.0%; Score 152; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYKISTEIKGVIVRIETILP 30
Db 1 DAEFRHDSGYKISTEIKGVIVRIETILP 30

RESULT 2
AAE35678 ID AAE35678 standard; peptide; 32 AA.

AC AAE35678;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
XX vaccine; nontropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
XX Measles virus.
XX Chimeric.

OS Key Location/Qualifiers

FT Region 1..12
FT /note= "Human beta amyloid peptide"

FT Region 16..32
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
XX fragment of amyloid beta peptide linked to the epitope, and optionally a
XX spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9, Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a

CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 32 AA;

Query Match 92.8%; Score 141; DB 6; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.3e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DAEFRHDSGY--KISTEIKGVIVRIETILP 30
Db 1 DAEFRHDSGYKISTEIKGVIVRIETILP 32

RESULT 3
AAE35679 ID AAE35679 standard; peptide; 34 AA.

AC AAE35679;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
XX vaccine; nontropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
XX Measles virus.
XX Chimeric.

OS Key Location/Qualifiers

FT Region 1..14
FT /note= "Human beta amyloid peptide"

FT Region 18..34
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
XX fragment of amyloid beta peptide linked to the epitope, and optionally a
XX spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9, Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 34 AA;

Query Match 92.1%; Score 140; DB 6; Length 34;
Best Local Similarity 88.2%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 DAEPFRHDSGY-----KISTIRIKGVYHRIETILF 30
Db 1 DAEPFRHDSGYEVHQRKLVFPAPDVGSNKKISTIRIKGVYHRIETILF 34

RESULT 4

AAE35680 standard; peptide; 48 AA.

AAE35680;

AC 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.

Immunogen: helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

Key Location/Qualifiers

PH 1..28
FT /note= "Human beta amyloid peptide"
FT Region 32..48
FT /note= "Measles virus T helper cell epitope"

W0200296350-A2.

05-DEC-2002.

02-APR-2002; 2002W0-US010293.

25-MAY-2001; 2001US-00865294.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI: 2003-201258/19.

Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
fragment of amyloid beta peptide linked to the epitope, and optionally a
spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9; Page 39; 77pp; English.

PS The present invention relates to a novel peptide immunogen comprising a
XX helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SQ Sequence 48 AA;

Query Match 87.5%; Score 133; DB 6; Length 48;
Best Local Similarity 62.5%; Pred. No. 2.5e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

QY 1 DAEPFRHDSGY-----KISTIRIKGVYHRIETILF 30
Db 1 DAEPFRHDSGYEVHQRKLVFPAPDVGSNKKISTIRIKGVYHRIETILF 48

RESULT 5

AAE35681 standard; peptide; 34 AA.

AAE35681;

AC 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.

Immunogen: helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

Key Location/Qualifiers

PH 1..14
FT /note= "Human beta amyloid peptide"
FT Region 18..34
FT /note= "Measles virus T helper cell epitope"

W0200296350-A2.

05-DEC-2002.

02-APR-2002; 2002W0-US010293.

25-MAY-2001; 2001US-00865294.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI: 2003-201258/19.

Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
fragment of amyloid beta peptide linked to the epitope, and optionally a
spacer, useful for preventing or treating Alzheimer's disease.

PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
PS Disclosure; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 34 AA:
XX
Query Match 82.9%; Score 126; DB 6; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.1e-12;
Matches 27; Conservative 2; Mismatches 1; Indels 4; Gaps 1;
XX
QY 1 DAEPFRDGGY----KISITIKGVVHRIETTLF 30
DB 1 DAEPFRDGGYVHNKISITIKGVVHRIETTLF 34
XX
RESULT 6
AAB35682
ID AAB35682 standard; peptide; 34 AA.
XX
AC AAB35682;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DB Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
PH Key 1. 14 Location/Qualifiers
PH Region /note= "Human beta amyloid peptide"
FT 18. .34
FT Region /note= "Measles virus T helper cell epitope"
XX
FN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PP 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.

XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
PS Disclosure; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 34 AA:
XX
Query Match 78.3%; Score 119; DB 6; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.6e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
XX
QY 1 DAEPFRDGGY----KISITIKGVVHRIETTLF 30
DB 1 DAEPFRDGGYVHNKISITIKGVVHRIETTLF 34
XX
RESULT 7
AAB35657
ID AAB35657 standard; peptide; 19 AA.
XX
AC AAB35657;
XX
DT 17-JUN-2003 (first entry)
DT 17-JUN-2003 (first entry)
XX
DB Measles virus T helper cell epitope #31.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic.
XX
OS Measles virus.
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PP 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
PS Claim 1; Page 37; 77pp; English.
XX

CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domain. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention

SQ Sequence 19 AA;

Query Match 59.2%; Score 90; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISTTRIKGVIVHRIETLP 30
DB 1 ISTTRIKGVIVHRIETLP 19

RESULT 8
ADD89946
ID ADD89946 standard; protein; 31 AA.

AC ADD89946;
XX
DT 29-JAN-2004 (first entry)

DE CD4 peptide used in immunostimulant complex for anti-HIV vaccine.

KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.

OS Synthetic.
XX Homo sapiens.

PH Key Location/Qualifiers
FT Modified-site 20
XX /note= "Bpsilon-lysine"

PN MO2003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003MO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

DR WPI, 2003-778890/73.

XX Stabilized immunostimulating complex, useful for vaccination, e.g.
XX against human immune deficiency viruses, comprises cationic peptide
XX immunogen and anionic oligonucleotide.

PS Claim 14; SEQ ID NO 6; 159pp; English.

XX The present sequence is that of a synthetic immunogenic peptide derived
XX from human CD4. This is an example of peptides that can be used in
XX claimed immunostimulatory complexes of the invention that are
XX specifically adapted to act as adjuvant and as peptide immunogen

CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present CD4 derived peptide can be used in an anti-
CC CD4 immunotherapeutic vaccine for the treatment of HIV infection.

SQ Sequence 31 AA;

Query Match 59.2%; Score 90; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISTTRIKGVIVHRIETLP 30
DB 1 ISTTRIKGVIVHRIETLP 19

RESULT 9
ADD89951
ID ADD89951 standard; protein; 45 AA.

AC ADD89951;
XX
DT 29-JAN-2004 (first entry)

DE Igb peptide used in immunostimulant complex for allergy vaccine.

KW Immunostimulant; vaccine; human; immunogen; Igb; immunotherapy; allergy;

KM antibody; antiallergic.

OS Synthetic.
XX Homo sapiens.

PH Key Location/Qualifiers
FT Modified-site 20
XX /note= "Bpsilon-lysine"

PN MO2003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003MO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

DR WPI, 2003-778890/73.

XX Stabilized immunostimulating complex, useful for vaccination, e.g.
XX against human immune deficiency viruses, comprises cationic peptide
XX immunogen and anionic oligonucleotide.

PS Claim 20; SEQ ID NO 11; 159pp; English.

XX The present sequence is that of a synthetic immunogenic peptide derived
XX from human Igb. This is an example of peptides that can be used in
XX claimed immunostimulatory complexes of the invention that are
XX specifically adapted to act as adjuvant and as peptide immunogen
XX stabiliser. The complexes comprise a CpG oligonucleotide and a
XX biologically active peptide immunogen. The complex is particulate and can
XX efficiently present peptide immunogens to the cells of the immune system
XX to produce an immune response. The complexes may be prepared with various
XX ratios of peptides to CpG oligonucleotides to provide different physical
XX properties, such as the size of the microparticle. An immunostimulatory
XX complex comprising the present Igb derived peptide can be used in an anti-
XX Igb immunotherapeutic vaccine for the treatment of allergy.

```
XX Sequence 45 AA;
SQ
Query Match 59.2%; Score 90; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVRIETILF 30
Db 1 ISITEIKGVIVRIETILF 19

RESULT 10
ADD89944 ID ADD89944 standard; protein; 50 AA.
AC ADD89944;
XX
DT 29-JAN-2004 (first entry)
XX
DB CD4 peptide used in immunostimulant complex as anti-HIV vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 20 /note="Epsilon-lysine"
XX
XX WO2003068169-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003MO-US004711.
XX
XX 14-FEB-2002; 2002US-00076674.
XX
XX 31-JAN-2003; 2003US-00076674.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX PA
XX PI Sokoll KK;
XX
XX WPI; 2003-778890/73.
XX
XX Stabilized immunostimulating complex, useful for vaccination, e.g.
XX PT against human immune deficiency viruses, comprises cationic peptide
XX immunogen and anionic oligonucleotide.
XX
XX Claim 14; SEQ ID NO 4; 159pp; English.
XX
XX The present sequence is that of a synthetic immunogenic peptide derived
XX from human CD4. This is an example of peptides that can be used in
XX claimed immunostimulatory complexes of the invention that are
XX specifically adapted to act as adjuvant and as peptide immunogen
XX stabiliser. The complexes comprise a Cpg oligonucleotide and a
XX biologically active peptide immunogen. The complex is particulate and can
XX efficiently present peptide immunogens to the cells of the immune system
XX to produce an immune response. The complexes may be prepared with various
XX ratios of peptides to Cpg oligonucleotides to provide different physical
XX properties, such as the size of the microparticle. An immunostimulatory
XX complex comprising the present CD4 derived peptide can be used in an anti
XX -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
XX Sequence 50 AA;
SQ
Query Match 59.2%; Score 90; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVRIETILF 30
Db 1 ISITEIKGVIVRIETILF 30
```

```
Db 1 ISITEIKGVIVRIETILF 19

RESULT 11
ADD89953 ID ADD89953 standard; protein; 65 AA.
AC ADD89953;
XX
DT 29-JAN-2004 (first entry)
XX
DB Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX Foot-and-mouth disease.
XX
KW Immunostimulant; vaccine; immunogen; immunotherapy;
XX Foot-and-mouth disease.
XX
OS Synthetic.
OS Foot-and-mouth disease virus.
XX
FH Key Location/Qualifiers
FT Modified-site 20 /note="Epsilon-lysine"
XX
XX WO2003068169-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003MO-US004711.
XX
XX 14-FEB-2002; 2002US-00076674.
XX
XX 31-JAN-2003; 2003US-00076674.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX PA
XX PI Sokoll KK;
XX
XX WPI; 2003-778890/73.
XX
XX Stabilized immunostimulating complex, useful for vaccination, e.g.
XX PT against human immune deficiency viruses, comprises cationic peptide
XX immunogen and anionic oligonucleotide.
XX
XX Claim 22; SEQ ID NO 13; 159pp; English.
XX
XX The present sequence is that of a synthetic immunogenic peptide derived
XX from foot-and-mouth disease (FMD) virus. This is an example of peptides
XX that can be used in claimed immunostimulatory complexes of the invention
XX that are specifically adapted to act as adjuvant and as peptide immunogen
XX stabiliser. The complexes comprise a Cpg oligonucleotide and a
XX biologically active peptide immunogen. The complex is particulate and can
XX efficiently present peptide immunogens to the cells of the immune system
XX to produce an immune response. The complexes may be prepared with various
XX ratios of peptides to Cpg oligonucleotides to provide different physical
XX properties, such as the size of the microparticle. An immunostimulatory
XX complex comprising the present FMD virus derived peptide can be used in
XX an anti-FMD vaccine for protective immunity against FMD.
XX
XX Sequence 65 AA;
SQ
Query Match 57.2%; Score 87; DB 7; Length 65;
Best Local Similarity 94.7%; Pred. No. 6.5e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVRIETILF 30
Db 1 ISITEIKGVIVRIETILF 19

RESULT 12
ADD89952 ID ADD89952 standard; protein; 65 AA.
AC ADD89952;
```

XX 29-JAN-2004 (first entry)
 DT Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
 XX
 XX Immunostimulant; vaccine; immunogen; immunotherapy;
 KW foot-and-mouth disease.
 XX
 XX Synthetic.
 OS Foot-and-mouth disease virus.
 XX
 XX Key Location/Qualifiers
 PH Modified-site 20
 FT /note= "Epsilon-lysine"
 FT
 XX WO2003068169-A2.
 PN
 XX 21-AUG-2003.
 XX
 XX 14-FEB-2003; 2003WO-US004711.
 PF
 XX 14-FEB-2003; 2002US-00076674.
 PR 31-JAN-2003; 2003US-00076674.
 XX
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA
 XX Sokolj KK;
 PI
 XX WPI; 2003-778890/73.
 DR
 XX Stabilised immunostimulating complex, useful for vaccination, e.g.
 PT against human immune deficiency viruses, comprises cationic peptide
 PT immunogen and anionic oligonucleotide.
 PT
 PS Claim 22; SEQ ID NO 12; 159pp; English.
 XX
 XX The present sequence is that of a synthetic immunogenic peptide derived
 CC from foot-and-mouth disease (FMD) virus. This is an example of peptides
 CC that can be used in claimed immunostimulatory complexes of the invention
 CC that are specifically adapted to act as adjuvant and as peptide immunogen
 CC stabiliser. The complexes comprise a Cpg oligonucleotide and a
 CC biologically active peptide immunogen. The complex is particulate and can
 CC efficiently present peptide immunogens to the cells of the immune system
 CC to produce an immune response. The complexes may be prepared with various
 CC ratios of peptides to Cpg oligonucleotides to provide different physical
 CC properties, such as the size of the microparticle. An immunostimulatory
 CC complex comprising the present FMD virus derived peptide can be used in
 CC an anti-FMD vaccine for protective immunity against FMD.
 CC
 CC Sequence 65 AA:
 SQ
 Query Match 54.6%; Score 83; DB 7; Length 65;
 Best Local Similarity 89.5%; Pred. No. 2.8e-05;
 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 ISTRIKGVIRIETILP 30
 Db 1 ISISIKGVIRIETILP 19
 RESULT 13
 ID AAY91268 standard; peptide; 31 AA.
 AC AAY91268;
 XX
 XX 12-SEP-2003 (revised)
 DT 22-MAY-2000 (first entry)
 XX
 XX Modified MVF Th epitope/HIV epitope. SEQ ID NO:146.
 DR Promiscuous T-cell epitope; measles virus F protein; MVF;
 XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW

KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 XX Measles virus.
 OS Human immunodeficiency virus 1.
 OS Chimeric.
 XX
 XX WO9966957-A2.
 PN
 XX 29-DEC-1999.
 PD
 XX 21-JUN-1999; 99WO-US013975.
 PF
 XX 20-JUN-1998; 98US-00100412.
 PR
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA
 XX Wang CY;
 PI
 XX WPI; 2000-160564/14.
 DR
 XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and immunocastration)
 CC ; for promoting the growth of animals; or for treating allergies or
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
 CC genetically diverse subjects) into an immunogen improves capacity to
 CC induce a strong T helper cell-mediated immune response, resulting in
 CC production of antibodies against a target antigen. Th can replace carrier
 CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
 CC represents a promiscuous T helper epitope from the measles virus F (MVF)
 CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
 CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
 CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
 CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
 CC epitope. Somatostatin immunogens may be used to promote growth in
 CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
 CC AAY91209-Y90211 are MVN Th epitope/CD4 CDR2 domain antigenic peptides which may
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified
 CC version of a human IgG (immunoglobulin B) CH3 domain, and AAY90213-Y90219
 CC are Th epitope/IgB CH3 antigenic peptides which may be used in the
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
 CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
 CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
 CC AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are
 CC immunogens comprising a CERP peptide and a Th epitope which may be used
 CC to prevent or treat arteriosclerosis and cardiovascular diseases. AAY91247
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-

CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
 CC invasive protein epitope from *Yersinia* species, and hinge spacer peptide,
 CC both of which may optionally be used in the antigenic peptides of the
 CC invention. (Updated on 12-SEP-2003 to standardise OS field)
 CC XX
 SO Sequence 31 AA:
 Query Match 53.0%; Score 80.5; DB 3; Length 31;
 Best Local Similarity 72.0%; Pred. No. 2.7e-05;
 Matches 18; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
 QY 6 HDGKSTIRKGVYHRTILF 30
 DB 8 HES-WXISIRKGVYHRTILF 31
 RESULT 14
 ID AAY91260 standard; peptide; 29 AA.
 XX AAY91260;
 AC AAY91260;
 XX 12-SEP-2003 (revised)
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified WVF Th epitope/HIV epitope, SEQ ID NO:138.
 XX Promiscuous T-cell epitope; measles virus F protein; WVF;
 XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CPTP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Measles virus.
 OS Human immunodeficiency virus 1.
 OS Chimeric.
 OS WO9966957-A2.
 PN WO9966957-A2.
 XX 29-DEC-1999.
 PD 29-DEC-1999.
 XX 21-JUN-1999; 99MO-US013975.
 PF 21-JUN-1999; 99MO-US013975.
 XX 20-JUN-1998; 98US-00100412.
 PR 20-JUN-1998; 98US-00100412.
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus.
 PT
 PS Claim 13; Page 63; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and immunocastration)

CC ; for promoting the growth of animals; or for treating allergies or
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
 CC genetically diverse subjects) into an immunogen improves capacity to
 CC induce a strong T helper cell-mediated immune response, resulting in
 CC production of antibodies against a target antigen. Th can replace carrier
 CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
 CC represents a promiscuous T helper epitope from the measles virus F (MVF)
 CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
 CC represent synthetic Th epitopes based on the WVF Th epitope. Sequence
 CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
 CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
 CC epitope. Somatostatin immunogens may be used to promote growth in
 CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
 CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified
 CC version of a human IGR (immunoglobulin B) CH3 domain, and AAY90213-Y90219
 CC are Th epitope/IgB CH3 antigenic peptides which may be used in the
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
 CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
 CC antigen and an WVF Th epitope and may be used in a malaria vaccine.
 CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
 CC immunogens comprising a CETP peptide and a Th epitope which may be used
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
 CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
 CC invasive protein epitope from *Yersinia* species, and hinge spacer peptide,
 CC both of which may optionally be used in the antigenic peptides of the
 CC invention. (Updated on 12-SEP-2003 to standardise OS field)
 CC XX
 SO Sequence 29 AA:
 Query Match 51.3%; Score 78; DB 3; Length 29;
 Best Local Similarity 77.3%; Pred. No. 6e-05;
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 GYKSTIRKGVYHRTILF 30
 DB 8 GPXISIRKGVYHRTILF 29
 RESULT 15
 ID AAY68551 standard; peptide; 19 AA.
 XX AAY68551
 AC AAY68551;
 XX 05-MAY-2000 (first entry)
 DT 05-MAY-2000 (first entry)
 XX
 DE Helper T cell epitope derived from SSAL Th1.
 XX
 CC Structured synthetic antigen library; SSAL; helper T cell epitope;
 KM SSAL Th1; F protein; Measles virus; peptide immunogen; LHRH;
 KM luteinising hormone-releasing hormone; spermatogenesis; ovulation;
 KM oestrus; sexual development; sex hormone; promiscuous T helper epitope;
 KM vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
 KM breast cancer; endometriosis; boar taint; meat quality; immunocastration.
 XX
 OS Synthetic.
 OS Measles virus.
 OS WO9966952-A1.
 PN WO9966952-A1.
 XX 29-DEC-1999.
 PD 29-DEC-1999.
 XX

PF 21-JUN-1999; 99WO-US013960.
XX
PR 20-JUN-1998; 98US-00100414.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR MPI; 2000-160562/14.

XX New peptide immunogen containing luteinizing hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer.

PS Claim 1; Page 29; 102pp; English.

XX The present sequence represents a helper T cell epitope derived from a
CC structured synthetic antigen library (SSAL) helper T cell epitope
CC designated SSAL Th1. SSAL Th1 is modelled after a promiscuous epitope
CC taken from the P protein of the Measles virus. The present epitope is
CC designed to be used in tandem with a target antigen, luteinizing hormone-
CC releasing hormone (LHRH). The epitope is used to construct peptide
CC immunogens of the invention, which contain at least one antigenic target
CC site, i.e. luteinizing hormone-releasing hormone (LHRH) or its analogue,
CC and an artificial helper T cell epitope (Th). The peptide immunogens
CC cause induction of a specific immune response to LHRH which is involved
CC in regulation of spermatogenesis, ovulation, oestrus, sexual development
CC and secretion of sex hormones. Provision of a promiscuous T helper
CC epitope (which is functional in genetically diverse subjects) provides
CC optimum immunogenicity to the B cell epitopes of the target antigen and
CC thus high antibody titres against the target antigen. The peptide
CC immunogens of the invention are used to vaccinate against mammalian LHRH,
CC for use as (reversible) contraceptive; control of hormone-dependent
CC tumours (cancer of prostate or breast; also endometriosis); to prevent
CC boar taint (and improve meat quality) and for immunocastration

XX Sequence 19 AA;

Query Match 50.0%; Score 76; DB 3; Length 19;

Best Local Similarity 84.2%; Pred. No. 7.2e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 12 ISITRIKGIYVHRIETILP 30
||:|||||||:||||
DB 1 ISIRIKGIYVHRIETILP 19

Search completed: June 18, 2004, 19:58:51
Job time : 43.2515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 11.7791 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-71

Perfect score: 152
Sequence: 1 DAEFRHDSGKYSITEIKGVVHRIETILF 30Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued Patents AA:*
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2: /cgn2_6/pcodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/pcodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/pcodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/pcodata/2/iaa/PCUTS_COMB.pep:*
6: /cgn2_6/pcodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	50.0	19	3	US-09-100-414B-15 Sequence 15, Appl
2	76	50.0	19	4	US-09-303-323-15 Sequence 15, Appl
3	76	50.0	19	4	US-09-770-014-15 Sequence 15, Appl
4	76	50.0	31	3	US-09-100-414B-53 Sequence 53, Appl
5	76	50.0	31	3	US-09-303-323-53 Sequence 53, Appl
6	76	50.0	31	4	US-09-770-014-53 Sequence 53, Appl
7	76	50.0	35	3	US-09-100-414B-80 Sequence 80, Appl
8	76	50.0	35	3	US-09-303-323-80 Sequence 80, Appl
9	76	50.0	35	4	US-09-770-014-80 Sequence 80, Appl
10	76	50.0	46	3	US-09-100-414B-96 Sequence 96, Appl
11	76	50.0	46	3	US-09-303-323-96 Sequence 96, Appl
12	76	50.0	46	4	US-09-770-014-96 Sequence 96, Appl
13	76	50.0	47	3	US-09-100-414B-60 Sequence 60, Appl
14	76	50.0	47	3	US-09-303-323-60 Sequence 60, Appl
15	76	50.0	47	4	US-09-770-014-60 Sequence 60, Appl
16	76	50.0	49	3	US-09-100-414B-57 Sequence 57, Appl
17	76	50.0	49	3	US-09-303-323-57 Sequence 57, Appl
18	76	50.0	49	4	US-09-770-014-57 Sequence 57, Appl
19	76	50.0	80	3	US-09-100-600A-30 Sequence 30, Appl
20	76	46.7	19	3	US-09-100-414B-17 Sequence 17, Appl
21	76	46.7	19	3	US-09-303-323-17 Sequence 17, Appl
22	76	46.7	19	4	US-09-770-014-17 Sequence 17, Appl
23	76	46.7	31	3	US-09-100-414B-55 Sequence 55, Appl
24	76	46.7	31	3	US-09-303-323-55 Sequence 55, Appl
25	76	46.7	31	4	US-09-770-014-55 Sequence 55, Appl
26	69	45.4	19	3	US-09-100-414B-18 Sequence 18, Appl
27	69	45.4	19	3	US-09-100-414B-19 Sequence 19, Appl

28	69	45.4	19	3	US-09-100-414B-20 Sequence 20, Appl
29	69	45.4	19	3	US-09-303-323-18 Sequence 18, Appl
30	69	45.4	19	3	US-09-303-323-19 Sequence 19, Appl
31	69	45.4	19	3	US-09-303-323-20 Sequence 20, Appl
32	69	45.4	19	4	US-09-770-014-18 Sequence 18, Appl
33	69	45.4	19	4	US-09-770-014-19 Sequence 19, Appl
34	69	45.4	19	4	US-09-770-014-20 Sequence 20, Appl
35	69	45.4	31	3	US-09-100-414B-56 Sequence 56, Appl
36	69	45.4	31	3	US-09-100-414B-59 Sequence 59, Appl
37	69	45.4	31	3	US-09-100-414B-61 Sequence 61, Appl
38	69	45.4	31	3	US-09-303-323-56 Sequence 56, Appl
39	69	45.4	31	3	US-09-303-323-59 Sequence 59, Appl
40	69	45.4	31	3	US-09-303-323-61 Sequence 61, Appl
41	69	45.4	31	4	US-09-770-014-56 Sequence 56, Appl
42	69	45.4	31	4	US-09-770-014-59 Sequence 59, Appl
43	69	45.4	31	4	US-09-770-014-61 Sequence 61, Appl
44	69	45.4	35	3	US-09-100-414B-81 Sequence 81, Appl
45	69	45.4	35	3	US-09-303-323-81 Sequence 81, Appl

ALIGNMENTS

```
RESULT 1
US-09-100-414B-15
; Sequence 15, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-15

Query Match 50.0%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 ISITEIKGVVHRIETILF 30
DB 1 ISITEIKGVVHRIETILF 19

RESULT 2
```

US-09-303-323-15
Sequence 15, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-15

Query Match 50.0%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ISITIKGVYHRIETLP 30
|||:|||||||:||||
Db 1 ISITIKGVYHRIETLP 19

RESULT 3
US-09-770-014-15
Sequence 15, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-15

Query Match 50.0%; Score 76; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ISITIKGVYHRIETLP 30
|||:|||||||:||||
Db 1 ISITIKGVYHRIETLP 19

RESULT 4
US-09-100-414B-53
Sequence 53, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-53

Query Match 50.0%; Score 76; DB 3; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.7e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      12 ISITEIKGVIHRIETILF 30
        |||:|||||:||||
Db       1 ISISEIKGVIHKEIGILF 19
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RESULT 5
US-09-303-323-53
; Sequence 53, Application US/09303323
; Date of No. 5328887

GENERAL INFORMATION:
APPLICANT: Wang, Chang yi
TITLE OF INVENTION: NOVEL LHRH PETIDED
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York

```

;
;      ZIP: 10154-0054
;
;      COMPUTER READABLE FORM:
;
;      MEDIUM TYPE: Floppy disk
;
;      COMPUTER: IBM PC compatible
;
;      OPERATING SYSTEM: PC Windows
;
;      SOFTWARE: Word 97
;

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CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/09/303,323
FILING DATE:  30-APR-1999
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/100,414
 ; FILING DATE: 20-JUNE-1998
 ; ATTORNEY/AGENT INFORMATION:
 ;

NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 1-1000

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; LENGTH: 31 amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-53

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```
Query Match      50.0%; Score 76; DB 3; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.7e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```

Oy      12  ISITEIKGVIVHRIETILF 30
          |||:|||||||:||||
Db      1  ISISEIKGVIVHKEIGILF 15

```

RESULT 6
US-09-770-014-53
Sequence 53, Application US/09770014

PATENT NO.: 6539282
 GENERAL INFORMATION:
 APPLICANT: Wang, Chang yi
 TITLE OF INVENTION: NOVEL LHRH PEPTIDES
 TITLE OF INVENTION: IMINOGENS
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Flannegan, L.L.P.

```

10      IIP: 10154-0054
11      COMPUTER READABLE FORM:
12      MEDIUM TYPE: Floppy disk
13      COMPUTER: IBM PC compatible
14      OPERATING SYSTEM: PC Windows
15      SOFTWARE: Word 97
16      CURRENT APPLICATION DATA:
17      APPLICATION NUMBER: US/09/770,014
18      FILING DATE:
19      CLASSIFICATION:
20      PRIOR APPLICATION DATA:
21      APPLICATION NUMBER: 09/100,414
22      FILING DATE: 20-JUNE-1998
23      ATTORNEY/AGENT INFORMATION:
24      NAME: Maria H. Lin
25      REGISTRATION NUMBER: 29,323
26      REFERENCE/DOCKET NUMBER: 1151-4155
27      TELECOMMUNICATION INFORMATION:
28      TELEPHONE: 212-758-4800
29      TELEFAX: 212-751-6849
30      INFORMATION FOR SEQ ID NO: 53:
31      SEQUENCE CHARACTERISTICS:
32          LENGTH: 31 amino acids
33          TYPE: amino acid
34          TOPOLOGY: linear
35      MOLECULE TYPE: peptide
36      US-09-770-014-53

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Query Match 50.0%; Score 76; DB 4; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.7e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	12	ISTBIKGVIRHRIITLF	30
		: :	
Db	1	ISISBIKGVIRHKIBGLF	19

RESULT 7
US-09-100-414B-80
Sequence 80, Application US/09100414B

1 PATENT NO. 602348
 2 GENERAL INFORMATION:
 3 APPLICANT: Wang, Chang yi
 4 TITLE OF INVENTION: NOVEL LRR PEPTIDE
 5 TITLE OF INVENTION: IMMUNOGENS
 6 NUMBER OF SEQUENCES: 106
 7 CORRESPONDENCE ADDRESS:
 8 ADDRESS: Morgan & Plimegan, L.L.P.
 9

```

1 STREET: 345 Park Avenue
2 CITY: New York
3 STATE: NY
4
5 COUNTRY: USA
6
7 ZIP: 10154-0054
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPETER: IBM PC compatible
12 OPERATING SYSTEM: PC Windows
13
14 SOFTWARE: Word 97
15

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/100,414B
3 FILING DATE: 20-JUNE-1998
4 CLASSIFICATION: 424
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Maria H. Ilin
7 REGISTRATION NUMBER: 29,323
8 REFERENCE/POCKET NUMBER: 1151-415
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 212-758-4800
11 TELEFAX: 212-751-6849
12 INFORMATION FOR SEQ ID NO: 80:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 35 amino acids
15 TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-80

Query Match 50.0%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ISITIKGVYHRIETILP 30
Db 1 ISISIKGVYHRIETILP 19

RESULT 8

US-09-303-323-80
Sequence 80, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-80

Query Match 50.0%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ISITIKGVYHRIETILP 30
Db 1 ISISIKGVYHRIETILP 19

RESULT 9

US-09-770-014-80
Sequence 80, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-80

Query Match 50.0%; Score 76; DB 4; Length 35;
Best Local Similarity 84.2%; Pred. No. 2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ISITIKGVYHRIETILP 30
Db 1 ISISIKGVYHRIETILP 19

RESULT 10

US-09-100-414B-96
Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 50.0%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 ISITKIGVYVHRIETILF 30
DB 1 ISISIRKGVYVHKIGILF 19

RESULT 11
US-09-303-323-96

Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-96

Query Match 50.0%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 ISITKIGVYVHRIETILF 30
DB 1 ISISIRKGVYVHKIGILF 19

RESULT 12

US-09-770-014-96

Sequence 96, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-96

Query Match 50.0%; Score 76; DB 4; Length 46;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 ISITKIGVYVHRIETILF 30
DB 1 ISISIRKGVYVHKIGILF 19

RESULT 13

US-09-100-414B-60
Sequence 60, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-60

Query Match 50.0%; Score 76; DB 3; Length 47;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVHRIETIF 30
Db 17 ISISIKGVIVHRIEGLIF 35

RESULT 14
US-09-303-323-60
Sequence 60, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-60

Query Match 50.0%; Score 76; DB 3; Length 47;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVHRIETIF 30
Db 17 ISISIKGVIVHRIEGLIF 35

RESULT 15
US-09-770-014-60
Sequence 60, Application US/09770014
Patent No. 659282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-60

Query Match 50.0%; Score 76; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 2.8e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVHRIETIF 30
Db 17 ISISIKGVIVHRIEGLIF 35

Search completed: June 18, 2004, 20:04:45
Job time : 11.7791 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 33.865 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294A-71

Perfect score: 152
Sequence: 1 DAEFRHDSGYKISTEIKGVIVRIETILP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	152	100.0	30	10	US-09-865-294-71	Sequence 71, Appl
2	141	92.8	32	10	US-09-865-294-72	Sequence 72, Appl
3	140	92.1	34	10	US-09-865-294-73	Sequence 73, Appl
4	133	87.5	48	10	US-09-865-294-74	Sequence 74, Appl
5	126	82.5	34	10	US-09-865-294-75	Sequence 75, Appl
6	119	78.3	34	10	US-09-865-294-76	Sequence 76, Appl
7	90	59.2	19	10	US-09-865-294-51	Sequence 51, Appl
8	90	59.2	31	14	US-10-076-674-6	Sequence 6, Appl
9	90	59.2	31	15	US-10-355-161A-6	Sequence 6, Appl
10	90	59.2	45	14	US-10-076-674-11	Sequence 11, Appl
11	90	59.2	45	14	US-10-355-161A-11	Sequence 11, Appl
12	90	59.2	50	14	US-10-076-674-4	Sequence 4, Appl
13	90	59.2	50	15	US-10-355-161A-4	Sequence 4, Appl
14	87	57.2	65	15	US-10-355-161A-13	Sequence 13, Appl
15	83	54.6	65	15	US-10-355-161A-12	Sequence 12, Appl

16	76	50.0	19	10	US-09-747-802-49	Sequence 49, Appl
17	76	50.0	19	10	US-09-747-802-55	Sequence 55, Appl
18	76	50.0	19	10	US-09-865-294-38	Sequence 38, Appl
19	76	50.0	19	10	US-09-865-294-41	Sequence 41, Appl
20	76	50.0	19	10	US-09-865-294-47	Sequence 47, Appl
21	76	50.0	30	10	US-09-747-802-80	Sequence 80, Appl
22	76	50.0	32	10	US-09-747-802-82	Sequence 82, Appl
23	76	50.0	34	10	US-09-747-802-78	Sequence 78, Appl
24	76	50.0	39	10	US-09-747-802-84	Sequence 84, Appl
25	76	50.0	46	10	US-09-747-802-74	Sequence 74, Appl
26	76	50.0	46	10	US-09-747-802-76	Sequence 76, Appl
27	71	46.7	19	10	US-09-747-802-48	Sequence 48, Appl
28	71	46.7	19	10	US-09-865-294-40	Sequence 40, Appl
29	69	45.4	19	10	US-09-747-802-46	Sequence 46, Appl
30	69	45.4	19	10	US-09-747-802-50	Sequence 50, Appl
31	69	45.4	19	10	US-09-747-802-51	Sequence 51, Appl
32	69	45.4	19	10	US-09-747-802-54	Sequence 54, Appl
33	69	45.4	19	10	US-09-747-802-56	Sequence 56, Appl
34	69	45.4	19	10	US-09-865-294-42	Sequence 42, Appl
35	69	45.4	19	10	US-09-865-294-43	Sequence 43, Appl
36	69	45.4	19	10	US-09-865-294-46	Sequence 46, Appl
37	69	45.4	19	10	US-09-865-294-48	Sequence 48, Appl
38	69	45.4	30	10	US-09-747-802-81	Sequence 81, Appl
39	69	45.4	32	10	US-09-747-802-83	Sequence 83, Appl
40	69	45.4	34	10	US-09-747-802-85	Sequence 85, Appl
41	69	45.4	39	10	US-09-747-802-85	Sequence 85, Appl
42	69	45.4	46	10	US-09-747-802-75	Sequence 75, Appl
43	69	45.4	46	10	US-09-747-802-77	Sequence 77, Appl
44	64.5	42.4	35	9	US-09-972-475-15	Sequence 15, Appl
45	64.5	42.4	35	15	US-10-463-729-15	Sequence 15, Appl

ALIGNMENTS

```

RESULT 1
US-09-865-294-71
; Sequence 71, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-71

Query Match      100.0%: Score 152; DB 10; Length 30;
Best Local Similarity 100.0%: Pred. No. 1.6e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYKISTEIKGVIVRIETILP 30
DB      1 DAEFRHDSGYKISTEIKGVIVRIETILP 30

RESULT 2
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

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CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 72
LENGTH: 32
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-72

Query Match 92.8%; Score 141; DB 10; Length 32;
Best Local Similarity 93.8%; Pred. No. 9e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DAEFRHDSGY---KISTIRKGVIVHRIETILF 30
DB 1 DAEFRHDSGYEVHKKISTIRKGVIVHRIETILF 32

RESULT 3
US-09-865-294-73

Sequence 73, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease

FILE REFERENCE: 1151-4167

CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 73

LENGTH: 34

TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-73

Query Match 92.1%; Score 140; DB 10; Length 34;
Best Local Similarity 88.2%; Pred. No. 1.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 DAEFRHDSGY---KISTIRKGVIVHRIETILF 30
DB 1 DAEFRHDSGYEVHKKISTIRKGVIVHRIETILF 34

RESULT 4
US-09-865-294-74

Sequence 74, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease

FILE REFERENCE: 1151-4167

CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 74

LENGTH: 48

TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-74

Query Match 87.5%; Score 133; DB 10; Length 48;
Best Local Similarity 62.5%; Pred. No. 2.6e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

QY 1 DAEFRHDSGY---KISTIRKGVIVHRIETILF 30
DB 1 DAEFRHDSGYEVHKKISTIRKGVIVHRIETILF 48

RESULT 5
US-09-865-294-75

Sequence 75, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease

FILE REFERENCE: 1151-4167

CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 75

LENGTH: 34

TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-75

Query Match 82.9%; Score 126; DB 10; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.1e-12;
Matches 27; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 DAEFRHDSGY---KISTIRKGVIVHRIETILF 30
DB 1 DAEFRHDSGYEVHKKISTIRKGVIVHRIETILF 34

RESULT 6
US-09-865-294-76

Sequence 76, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease

FILE REFERENCE: 1151-4167

CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 76

LENGTH: 34

TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-76

Query Match 78.3%; Score 119; DB 10; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.7e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 DAEFRHDSGY---KISTIRKGVIVHRIETILF 30
DB 1 DAEFRHDSGYEVHKKISTIRKGVIVHRIETILF 34

RESULT 7
US-09-865-294-77

Sequence 77, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease

FILE REFERENCE: 1151-4167

CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 77

LENGTH: 19

TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-51

Query Match 59.2%; Score 90; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISITEIKGVIVHRIETILF 30
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 8

US-10-076-674-6
Sequence 6, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

Query Match 59.2%; Score 90; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISITEIKGVIVHRIETILF 30
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 9

US-10-355-161A-6
Sequence 6, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

Query Match 59.2%; Score 90; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISITEIKGVIVHRIETILF 30
DB 1 ISITEIKGVIVHRIETILF 19

DB 1 ISITEIKGVIVHRIETILF 19

RESULT 10

US-10-076-674-11
Sequence 11, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

Query Match 59.2%; Score 90; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISITEIKGVIVHRIETILF 30
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 11

US-10-355-161A-11
Sequence 11, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)-(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

Query Match 59.2%; Score 90; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ISITEIKGVIVHRIETILF 30
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 12

US-10-076-674-4
Sequence 4, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.

```

; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRF
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

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Query Match          59.2%; Score 90; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 ISITEIKGIVVRIITILF 30
Db      1 ISITEIKGIVVRIITILF 19

```

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RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRF
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

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```

Query Match          59.2%; Score 90; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      12 ISITEIKGIVVRIITILF 30
Db      1 ISITEIKGIVVRIITILF 19

```

```

RESULT 14
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13

```

```

; LENGTH: 65
; TYPE: PRF
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

```

```

Query Match          57.2%; Score 87; DB 15; Length 65;
Best Local Similarity 94.7%; Pred. No. 5.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 ISITEIKGIVVRIITILF 30
Db      1 ISITEIKGIVVRIITILF 19

```

```

RESULT 15
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 65
; TYPE: PRF
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

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Query Match          54.6%; Score 83; DB 15; Length 65;
Best Local Similarity 89.5%; Pred. No. 2.4e-05;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 ISITEIKGIVVRIITILF 30
Db      1 ISITEIKGIVVRIITILF 19

```

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Search completed: June 18, 2004, 20:23:46
Job time : 33.865 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 9.0184 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITIKGVVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	42.1	546	1 VGNZRL	cell fusion glycop
2	62	40.8	42	2 PM0512	beta-amyloid prote
3	62	40.8	57	2 B60045	Alzheimer's diseas
4	62	40.8	57	2 F60045	Alzheimer's diseas
5	62	40.8	57	2 G60045	Alzheimer's diseas
6	62	40.8	57	2 D60045	Alzheimer's diseas
7	62	40.8	57	2 A60045	Alzheimer's diseas
8	62	40.8	57	2 B60045	Alzheimer's diseas
9	62	40.8	82	2 PQ0438	Alzheimer's diseas
10	62	40.8	695	1 A49795	Alzheimer's diseas
11	62	40.8	770	1 Q8HUA4	Alzheimer's diseas
12	61	40.1	546	2 S47300	gene F protein - r
13	60	39.5	546	1 VGNZRL	cell fusion glycop
14	60	39.5	546	1 S5386	cell fusion protei
15	60	39.5	546	2 S47305	gene F protein - r
16	59.5	39.1	552	2 S47034	cell fusion protei
17	59	38.8	542	2 J02223	cell fusion glycop
18	59	38.8	662	1 VGNZCD	cell fusion glycop
19	59	38.8	662	1 S21382	cell fusion protei
20	58	38.2	282	2 PQ0376	cell fusion glycop
21	58	38.2	282	2 PQ0388	cell fusion glycop
22	58	38.2	534	1 J00274	cell fusion glycop
23	58	38.2	550	1 B48556	cell fusion glycop
24	58	38.2	553	1 VGNZRV	cell fusion glycop
25	58	38.2	631	1 VGNZPD	cell fusion glycop
26	58	38.2	631	1 A48346	cell fusion glycop
27	53	34.9	229	2 F86180	hypothetical prote
28	52	34.2	220	2 T00801	probable synaptobr
29	52	34.2	240	2 T47589	synaptobrevin-like

30	51	33.6	236	2 A90190	hypothetical prote
31	51	33.6	421	2 T33811	hypothetical prote
32	51	33.6	695	2 A27485	Alzheimer's diseas
33	51	33.6	695	2 S00550	Alzheimer's diseas
34	50	32.9	33	2 S23094	beta-amyloid prote
35	50	32.9	649	2 B38129	bo-type ubiquinol
36	49.5	32.6	219	2 D89923	endonuclease-like
37	49	32.2	112	2 S26221	cruciferin (clone
38	49	32.2	458	2 B83588	RNA helicase Dbpa
39	48.5	31.9	356	2 D96537	hypothetical prote
40	48.5	31.9	426	2 S76247	hypothetical prote
41	48.5	31.9	792	2 B71539	probable omp85 ana
42	48.5	31.9	792	2 H81693	outer membrane pro
43	48	31.6	175	2 D86180	hypothetical prote
44	48	31.6	221	2 F84741	probable synaptobr
45	48	31.6	497	2 A82545	two-component syst

ALIGNMENTS

RESULT 1
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N:Contains: fusion glycoprotein F1, fusion glycoprotein F2
C:Species: rinderpest virus
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C/Accession: A28921
R:Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A>Title: Fusion glycoprotein (F) of rinderpest virus; entire nucleotide sequence of the
A/Reference number: A28921; MUID:88219541; PMID:3285575
A/Accession: A28921

A/Molecule type: mRNA
A/Residues: 1-546 <TSU>
A/Cross-references: GB:M20870; MID:G333898; PID:AAA47399.1; PID:G333899
A/Genetics:
A/Gene: F
C/Superfamily: paramyxovirus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F:105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F:109-133/Domain: transmembrane #status predicted <TM1>
F:485-513/Domain: transmembrane #status predicted <TM2>
F:25-57/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.1%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.18;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
DB 283 SLSEIKGVVHRLSEVSY 300

RESULT 2
PM0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragme
A/Reference number: PM0512; MUID:93290653; PMID:7685598
A/Accession: PM0512
A/Molecule type: protein
A/Residues: 1-42 <SH1>
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i;
C/Keywords: alternative splicing; amyloid

Query Match 40.8%; Score 62; DB 2; Length 42;

Best Local Similarity 40.6%; Pred. No. 0.022;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 32

RESULT 3

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C/Species: Ovis sp. (sheep)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: B60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: B60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: EMBL:X56130

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.03;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 37

RESULT 4

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: F60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: F60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.03;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 37

RESULT 5

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: G60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: G60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: EMBL:X56126
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.03;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 37

RESULT 6

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: D60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: D60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: EMBL:X56124

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.03;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 37

RESULT 7

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C/Species: Canis lupus familiaris (dog)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: A60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: A60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

A/Cross-references: EMBL:X56125

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.03;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEVHMQKLVFPAEDVGSNKGAI 37

RESULT 8

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C/Species: Ursus maritimus (polar bear)

C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: B60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA9593.1; PID:92166
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knittz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 40.8%; Score 62; DB 2; Length 57;
 Best Local Similarity 40.6%; Pred. No. 0.03;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Query 1 DAEFRHDSGYK-----SITEIKGVIV 22
 DB 6 DAEFRHDSGYEVHKKLVFPADVGSNKALII 37

RESULT 9
 P00438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: P00438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A:Reference number: P00438; MUID:93075180; PMID:1445331
 A:Accession: P00438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnson, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knittz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 40.8%; Score 62; DB 2; Length 82;
 Best Local Similarity 40.6%; Pred. No. 0.045;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Query 1 DAEFRHDSGYK-----SITEIKGVIV 22
 DB 17 DAEFRHDSGYEVHKKLVFPADVGSNKALII 48

RESULT 10
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlany, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A>Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117; PMID:1905108
 A:Accession: A49795
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA6829.1; PID:9342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knittz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 40.8%; Score 62; DB 1; Length 695;
 Best Local Similarity 40.6%; Pred. No. 0.46;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Query 1 DAEFRHDSGYK-----SITEIKGVIV 22
 DB 597 DAEFRHDSGYEVHKKLVFPADVGSNKALII 628

RESULT 11
 ORHNA4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternative names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Containing: amyloid beta protein long, plaque form, amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A3260; A35486; I39452; I39453; I59562; A44
 466; A28583; A29302; A60805; J00038; S06121; A60355; A59011; A38384; S29076; S3852; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A>Title: The PreA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A>Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA1830.1; PID:9871360
 A>Note: alternative splice form APP(695)
 R:LaFauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAC13654.1; PID:9516074
 R:Johnson, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030; PMID:2675837
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:9178663; PIDN:AAA51768.1; PID:9178665
 R:Prelli, F.; Levy, B.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A>Note: 693-gln was found in DNA isolated from HCMA-D patients
 R:Toshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AAB59502.1; PID:9178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
 A:Molecule type: DNA
 A:Residues: 1-530, 'OMLMPVTPAPWBAVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AAB59501.1; PID:9178615
 R:Toshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991

Db 672 DAEFRHDSGYEVHQRXVLPFAEDVGSNKGAI 703

RESULT 12

S47300
 gene F protein - rinderpest virus
 C/Species: rinderpest virus
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
 C/Accession: S47300, PQ0865
 R/Baron, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
 submitted to the EMBL Data Library, March 1994
 A/Description: The complete nucleotide sequence of the fusion protein gene of the vaccinia
 A/Reference number: S47299
 A/Accession: S47300
 A/Molecule type: DNA
 A/Residues: 1-546 <EVA>
 A/Cross-references: EMBL:Z31656; NID:G535406; PIDN:CAA83482.1; PID:G535407
 R/Chamberlain, R.W.; Mamway, H.M.; Hockley, E.; Shatta, M.S.; Goatley, L.; Knowles, N.J.
 J. Gen. Virol. 74, 2775-2780, 1993
 A/Title: Evidence for different lineages of rinderpest virus reflecting their geographic
 A/Reference number: PQ0865; NCID:94103786; PMID:8277286
 A/Accession: PQ0865
 A/Molecule type: mRNA
 A/Residues: 86-191 <CHA>
 C/Genetics:
 A/Gene: F
 C/Superfamily: parainfluenza virus cell fusion protein
 C/Keywords: glycoprotein; membrane fusion; transmembrane protein

Query Match 40.1%; Score 61; DB 2; Length 546;
 Best Local Similarity 61.1%; Pred. No. 0.5;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
 DB 283 SLSEIKGVVHRLGVSY 300

RESULT 13

VANZNRK
 cell fusion glycoprotein precursor - rinderpest virus (strain Kabete 0)
 N/Contains: fusion glycoprotein F1, fusion glycoprotein F2
 C/Species: rinderpest virus
 C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
 C/Accession: A31051
 R/Hsu, D.; Yamataka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
 Virology 166, 149-153, 1988
 A/Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis
 A/Reference number: A31051; NCID:88322864; PMID:3413983
 A/Accession: A31051
 A/Molecule type: genomic RNA
 A/Residues: 1-546 <HSU>
 C/Genetics:
 A/Gene: F
 C/Superfamily: parainfluenza virus cell fusion protein
 C/Keywords: glycoprotein; membrane fusion; transmembrane protein
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-108/Product: cell fusion glycoprotein F2 #status predicted <FP1>
 F/109-546/Product: cell fusion glycoprotein F1 #status predicted <FP2>
 F/109-134/Domain: transmembrane #status predicted <TN2>
 F/491-513/Domain: transmembrane #status predicted <TN2>
 F/25,57,63,518/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.5%; Score 60; DB 1; Length 546;
 Best Local Similarity 55.6%; Pred. No. 0.7;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
 DB 283 SLSEIKGVVHRLGVSY 300

RESULT 14

S55386
 cell fusion protein - peste-des-petits-ruminants virus (strain 75/1)

N/Alternate names: F protein
 C/Species: peste-des-petits-ruminants virus
 A/Variety: strain 75/1
 C/Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
 C/Accession: S55386
 R/Meyer, G.; Diallo, A.
 submitted to the EMBL Data Library, September 1994
 A/Description: The nucleotide sequence of fusion protein gene of the Peste des petits r
 to each virus.
 A/Reference number: S55386
 A/Accession: S55386
 A/Molecule type: DNA
 A/Residues: 1-546 <MEY>
 A/Cross-references: EMBL:Z37017; NID:G854372; PIDN:CAA85451.1; PID:G854373
 A/Experimental source: strain 75/1; cell line vero
 C/Genetics:
 A/Gene: F
 C/Superfamily: parainfluenza virus cell fusion protein
 C/Keywords: membrane fusion

Query Match 39.5%; Score 60; DB 2; Length 546;
 Best Local Similarity 61.1%; Pred. No. 0.7;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
 DB 283 SLSEIKGVVHRLGVSY 300

RESULT 15

S47305
 gene F protein - rinderpest virus
 C/Species: rinderpest virus
 C/Date: 20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
 C/Accession: S47305; S47301
 R/Baron, M.D.; Barrett, T.
 submitted to the EMBL Data Library, March 1994
 A/Description: The sequence of the N and L genes of Rinderpest virus, and the 50 and 30
 A/Reference number: S47283
 A/Accession: S47305
 A/Molecule type: mRNA
 A/Residues: 1-546 <BAR>
 A/Cross-references: EMBL:Z30697; NID:G535396; PIDN:CAA83181.1; PID:G535401; EMBL:Z30700;
 C/Superfamily: parainfluenza virus cell fusion protein
 C/Keywords: transmembrane protein

Query Match 39.5%; Score 60; DB 2; Length 546;
 Best Local Similarity 55.6%; Pred. No. 0.7;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
 DB 283 SLSEIKGVVHRLGVSY 300

Search completed: June 18, 2004, 20:03:30
 Job time: 10.0184 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 5.88957 Seconds

(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-71

Perfect score: 152
Sequence: 1 DAEFRHDSGYKSTIEIKGVIRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	42.1	546	1	VGLE_RINDL
2	62	40.8	57	1	A4_URSWA
3	62	40.8	58	1	A4_CANFA
4	62	40.8	58	1	A4_RABIT
5	62	40.8	58	1	A4_SHEEP
6	62	40.8	59	1	A4_BOVIN
7	62	40.8	751	1	A4_SALIS
8	62	40.8	770	1	A4_CAVPO
9	62	40.8	770	1	A4_HUMAN
10	62	40.8	770	1	A4_MACPA
11	62	40.8	770	1	A4_PIG
12	61	40.1	546	1	VGLE_RINDB
13	60	39.5	546	1	VGLE_RINDR
14	59	38.8	662	1	VGLE_CDOVO
15	58	38.2	534	1	VGLE_MEASA
16	58	38.2	550	1	VGLE_MEASA
17	58	38.2	550	1	VGLE_MEASA
18	58	38.2	631	1	VGLE_PROD
19	54	35.5	546	1	VGLE_RINDK
20	53	34.9	229	1	V726_ARATH
21	52	34.2	220	1	V725_ARATH
22	52	34.2	240	1	V727_ARATH
23	51	33.6	235	1	PUR7_THRTN
24	51	33.6	770	1	A4_MOUSE
25	51	33.6	770	1	A4_RAT
26	50	32.9	529	1	VGLE_MEAST
27	50	32.9	649	1	COX1_BACSU
28	48.5	31.9	356	1	BCAA_ARATH
29	48	31.6	219	1	V721_ARATH
30	48	31.6	221	1	V722_ARATH
31	47.5	31.2	409	1	NQ04_THSTH
32	47.5	31.2	625	1	T954_HUMAN
33	47	30.9	264	1	DAEP_BACHD

34	47	30.9	571	1	DCP1_SCHPO
35	45	29.6	247	1	CAH_METTB
36	45	29.6	397	1	AAT_STRVG
37	45	29.6	488	1	CRU1_BRANA
38	45	29.6	490	1	CRU2_BRANA
39	45	29.6	496	1	CRU3_BRANA
40	45	29.6	680	1	OPDA_ECOLI
41	45	29.6	1005	1	MANA_DICDI
42	44.5	29.3	139	1	Y024_METUA
43	44.5	29.3	282	1	IF34_SCHPO
44	44.5	29.3	670	1	PBP_STRAU
45	44	28.9	260	1	Y338_METUA

ALIGNMENTS

RESULT 1	VGLE_RINDL	STANDARD;	PRT;	546 AA.
AC	P10864;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;			
DE	Fusion glycoprotein F1].			
GN	F			
OS	Rinderpest virus (strain L) (RDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Paramyxovirinae; Morbilliviruses.			
ON	NCBI_TaxID=11243;			
RX	MEDLINE=88219541; PubMed=3285575;			
RA	Tsukiyama K., Yoshikawa Y., Yamamouchi K.;			
RT	"Fusion glycoprotein (F) of rinderpest virus: entire nucleotide			
RT	sequence of the F mRNA, and several features of the F protein.";			
RL	Virology 164:523-530(1988).			
CC	- FUNCTION: This protein directs fusion of viral and cellular			
CC	membranes.			
CC	- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2			
CC	LINKED BY A DISULFIDE BOND.			
CC	- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein			
CC	family.			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M20870; AAA47393.1; -.			
DR	PIR; A28921; VGNZRL.			
DR	HSSP; P04849; ISVP.			
DR	InterPro; IPR000776; Fusion gly.			
DR	Pfam; PF00523; fusion gly; 1.			
KW	Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.			
FT	STGNAL 1			
FT	CHAIN 20 546			
FT	CHAIN 20 108			
FT	CHAIN 109 546			
FT	DOMAIN 104 108			
FT	TRANSMEM 109 133			
FT	TRANSMEM 484 513			
FT	DOMAIN 514 517			
FT	LINKAGE BETWEEN F2 & F1 (POTENTIAL).			
FT	DISULFID 64 191			
FT	CARBOHYD 25 25			
FT	CARBOHYD 57 57			
FT	CARBOHYD 63 63			
SO	SEQUENCE 546 AA; 58911 MW; 985029418F28F8P85 CRC64;			

Query	March	42.1%	Score 64	DB 1	Length 546
Best Local Similarity	61.1%	Pred. No. 0.067			
Matches	11	Conservative	6	Mismatches	1
				Indels	0
				Gaps	0
Qy	13	STRICKVIVHRIILF	30		
	::: :::				
Db	283	SLSEIKGVIVHLESVY	300		

```

RESULT 2
A4_URSMMA
ID_ A4_URSMMA STANDARD; PRT; 57 AA.
AC Q25149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 35, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-ApP) (A-Beta)] (Fragment) .
CN App.
OS Ursus maritimus (Polar bear) (Thalartos maritimus) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079, PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991) .
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (by similarity) .
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the ApP family.
CC -----
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CC -----
CC EMBL; X56128; CAA39593.1; -.
CC PIR; B60045; B60045.
CC HSSP; P05067; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR001255; Beta-ApP.
CC Pfam; PF03494; Beta-ApP.1.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON TER 1 1
CC FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL) .
CC FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL) .
CC FT TRANSMEM 34 57 POTENTIAL.
CC FT NON TER 57 57
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D88BBA2DFA CRC64;
Query Match 40.8%; Score 62; DB 1; Length 57;
Best Local Similarity 40.6%; Pred. No. 0.012;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1.
1 DAEFRHDSGYKI-----SITEINGIV 22
|||||:::|
6 DAEFRHDSGYEVHOKLVFPAEDVGSNKGAII 37

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ID A4 CANFA STANDARD; PRT; 58 AA.
AC Q2B280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 35, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DS protein (beta-APP) (A-beta)] (Fragment).
OS APP.
GN
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Kidney; N.A.
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris P.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X56125; CAA39590.1; -.
CC HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF0494; Beta-APP; 1.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurons; Transmembrane.
PT CHAIN 1
PT DOMAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
PT TRANSMEM 35 58 EXTRACELLULAR (POTENTIAL).
PT NON TER 58 POTENTIAL.
SQ SEQUENCE 58 AA; 6285 MW; 8469D48BA2E12DFA CRC64;

Query Match 40.8%; Score 62; DB 1; Length 58;
Best Local Similarity 40.6%; Pred. No. 0.012; 5; Indels 10; Gaps 1.
Matches 13; Conservative 4; Mismatches

QY 1 DAEPFHDSGYKI-----SITIKGVIV 22
ID 7 DAEPFHDSGYEVHMQKLVPAEDYGSNKGAI 38
ID A4 RABIT STANDARD; PRT; 58 AA.
AC Q2B748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DS protein (beta-APP) (A-beta)] (Fragment).
OS APP.
GN
NC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

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CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CC Eucaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9615;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RC MEDLINE=92017079; PubMed=1656157;
RX Johnstone E.M., Chaney M.O., Morris P.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor through the GTP-binding protein
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56125; CAA39590.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR Glycoprotein; Amyloid; Neurone; Transmembrane.
KW NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58
SQ SBOUENCE 58 AA; 6285 MW; 8456D48BA2B12DFA CRC64;

Query Match 40.8%; Score 62; DB 1; Length 58;
Best Local Similarity 40.6%; Pred. No. 0.012;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

QY 1 DAEFRHDSGYKI-----STETIKGVIV 22
   |||||:::|:|:|
DB 7 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAI 38

RESULT 4
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
OS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92011079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
-----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56129; CA39594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR01255; Beta-APP.
DR Pfam; PF03494; Beta-APP_1.
DR PROSITE; PS00319; A4_EXTRA: PARTIAL.
DR PROSITE; PS00320; A4_INTRA: PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 >58 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; P434209D88BBA82D CRC64;
Query March 40.8%; Score 62; DB 1; Length 58;
Best local Similarity 40.6%; Pred. No. 0.012;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
Qy 1 DAEFRHDSGYK-----SITEIKGVIV 22
Db 6 DAEFRHDSGYEHHQKVFPADVCSNKGALL 37
RESULT 5
AC A4_SHEEP STANDARD; PRT; 58 AA.
AC 028757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 35, Last annotation update)
DB Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-Beta)] (Fragment).
GN APP.
OS Ovis aries (sheep) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92011079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56129; CA39594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR01255; Beta-APP.
DR Pfam; PF03494; Beta-APP_1.
DR PROSITE; PS00319; A4_EXTRA: PARTIAL.
DR PROSITE; PS00320; A4_INTRA: PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 >58 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; P434209D88BBA82D CRC64;
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CC      intracellular signaling pathway through the GTP-binding protein
CC      G1O) (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: Belongs to the APP family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities require a license agreement (See http://www.isb-eb.ch/announce/
CC      or send an email to license@isb-eb.ch).
CC      -----
CC      EMBL; X56130; CA439595.1; -.
CC      DR      HSSP; P05067; 1BA4.
CC      DR      InterPro; IPR008155; A4 APP.
CC      DR      InterPro; IPR001255; Beta-APP.
CC      DR      Pfam; PF03494; Beta-APP; 1.
CC      DR      PROSITE; PS00319; A4-EXTRA; PARTIAL.
CC      DR      PROSITE; PS00320; A4-INTRA; PARTIAL.
CC      KM      Glycoprotein; Amyloid; Neutro; Transmembrane.
CC      FT      NON TER      1      1
CC      FT      CHAIN      6      48      BETA-AMYLOID PROTEIN (POTENTIAL).
CC      FT      DOMAIN      <1      33      EXTRACELLULAR (POTENTIAL).
CC      FT      TRANSMEM      34      57      POTENTIAL.
CC      FT      DOMAIN      58      58      CYTOPLASMIC (POTENTIAL).
CC      FT      NON TER      58      58
CC      SQ      SEQUENCE      58 AA; 6300 MW; F434209D88EBA82D CRC64;
CC
CC      Query Match      40.8%; Score 62; DB 1; Length 58;
CC      Basic Local Similarity      40.6%; Pred. No. 0.012;
CC      Matches      13; Conservative      4; Mismatches      5; Indels      10; Gaps      1;
CC
CC      Oy      1      DAERFHDGSGYKI-----SITTEIKGVIV 22
CC      Db      6      DAERFHDGSGYVHHQKLVPRFEDGSKKGLI 37
CC
CC      RESULT 6
CC      A4 BOVIN
CC      ID_ A4 BOVIN      STANDARD;      PRT;      59 AA.
CC      AC      Q26053;
CC      DT      01-NOV-1997 (Rel. 35, Created)
CC      DT      01-NOV-1997 (Rel. 35, Last sequence update)
CC      DT      30-MAY-2000 (Rel. 39, Last annotation update)
CC      DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
CC      DE      protein (Beta-APP) (A-beta)] (Fragment).
CC      GN      APP.
CC      OS      Bos taurus (Bovine).
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC      OC      Bovidae; Bovinae; Bos.
CC      OX      NCBI_TaxId=9913;
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A.
CC      RC      TISSUE=Brain;
CC      RX      MEDLINE=92017079; PubMed=1656157;
CC      RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC      RT      "Conservation of the sequence of the Alzheimer's disease amyloid
CC      RT      peptide in dog, polar bear and five other mammals by cross-species
CC      RT      polymerase chain reaction analysis.";
CC      RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      RL      -1- FUNCTION: Functional neuronal receptor which couples to
CC      CC      intracellular signaling pathway through the GTP-binding protein
CC      CC      G1O) (By similarity).
CC      CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      CC      -1- SIMILARITY: Belongs to the APP family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
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 DR EMBL; X56124; CAA39589.1; -
 CC DR EMBL; X56126; CAA39591.1; -
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR008155; A4-APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4-EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4-INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON TER 1
 FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 58 POTENTIAL.
 FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
 FT NON TER 59 59
 SQ SEQUENCE 59 AA; 6414 MW; P43469D48A2E12D CRC64;
 Query Match 40.8%; Score 62; DB 1; Length 59;
 Best Local Similarity 40.6%; Pred. No. 0.012;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
 1 DAEFRHDSGYK-----SITEIKGVV 22
 7 DAEFRHDSGYEVHOKLVPAEDVGSNKCAII 38
 RESULT 7
 ID_A4_SALISC STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DB protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DB APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
 DB Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DB CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DB (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DB secretase C-terminal fragment 50); C31].
 GN APP.
 OS Salmiiri scureaus (Common squirrel monkey).
 CC Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salmiiri.
 CC NCBI_Taxid=9521;
 RN [1]
 RP SOURCE FROM N.A.
 RC TISSUE: Kidney and Liver;
 RX MEDLINE=96108492; PubMed8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate low-
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By

CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, PP2B1, APPBP1, IBI, KNS2
 CC (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1.
 CC In vitro, it binds MAPT via the WT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via a clathrin-coated
 CC pit. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and

inhibits collagen-binding (By similarity).
 - SIMILARITY: Belongs to the APP family.
 - SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
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 EMBL: S61024; AAC14347.1; -
 HSP: P05067; IAP.
 InterPro: IPR008155; A4_APP.
 InterPro: IPR008154; A4_extra.
 InterPro: IPR001255; Beta-APP.
 InterPro: IPR002233; Kunitz_BPT1.
 Pfam: PF02177; A4_EXTRA; 1.
 Pfam: PF03494; Beta-APP; 1.
 Pfam: PF00014; Kunitz_BPT1; 1.
 PRINTS: PR00203; AMYLOIDA4.
 PRINTS: PR00759; BASICPTASR.
 ProDom: PD000222; Kunitz_BPT1; 1.
 SMART: SM00006; A4_EXTRA; 1.
 SMART: SM00131; KU; 1.
 PROSITE: PS00319; A4_EXTRA; 1.
 PROSITE: PS00320; A4_INTRA; 1.
 PROSITE: PS00280; BPT1_KUNITZ_1; 1.
 PROSITE: PS50229; BPT1_KUNITZ_2; 1.
 Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 Proteoglycan; Amyloid; Alternative splicing.
 BY SIMILARITY.
 SIGNAL. 1 17
 PT CHAIN 18 751
 PT CHAIN 18 668
 PT CHAIN 18 652
 PT CHAIN 653 751
 PT CHAIN 653 694
 PT CHAIN 653 692
 PT CHAIN 669 751
 PT CHAIN 669 694
 PT CHAIN 669 692
 PT CHAIN 693 751
 PT CHAIN 695 751
 PT CHAIN 702 751
 PT CHAIN 721 751
 PT CHAIN 18 680
 PT TRANSMEM 681 704
 PT DOMAIN 705 751
 PT DOMAIN 96 110
 PT DOMAIN 181 188
 PT DOMAIN 291 341
 PT DOMAIN 316 344
 PT DOMAIN 363 428
 PT DOMAIN 504 521
 PT DOMAIN 713 732
 PT DOMAIN 230 260
 PT DOMAIN 274 280
 PT SITE 144 144
 ACT SITE 301 302
 SITE 652 653
 SITE 653 654
 SITE 668 669
 SITE 685 685
 SITE 687 687

FT SITE 692 693 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 FT SITE 694 695 (BY SIMILARITY).
 FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 FT SITE 705 715 (BY SIMILARITY).
 FT SITE 720 721 BASOLATERAL SORTING SIGNAL
 FT SITE 738 741 (BY SIMILARITY).
 FT SITE 740 743 CLEAVAGE (BY CASPASE-3, -6, -8 OR -9)
 FT SITE 740 743 (BY SIMILARITY).
 FT SITE 740 743 ENDOCYTOSIS SIGNAL.
 FT SITE 740 743 NPXY MOTIF.
 Query Match 40.8%; Score 62; DB 1; Length 751;
 Best Local Similarity 40.6%; Pred. No. 0.19;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
 Qy 1 DAEFRHDSGYKI-----SITEIKGVIV 22
 Db 653 DAEFRHDSGYRHHQKLVFPAEDVGSNKGALI 684
 RESULT 8
 ID A4_CAVPO STANDARD; PRT; 770 AA.
 AC 060495; 060496;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 OS APP.
 GN Cavia porcellus (Guinea pig).
 OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBI_TaxID=10141;
 RN [1]
 RC TISSUE=Brain, and Liver;
 RC MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing."
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RC INTERACTION OF BETA-APP40 WITH APOE.
 RA Martel C.L., Mackic J.B., Matsubara B., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins B2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta."
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RC PROCESSING.
 RA MEDLINE=20064499; PubMed=10619481;
 RA Beck M., Breckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein."
 RL Neuroscience 95:243-254(2000).
 RN [4]
 RC GAMMA-SECRETASE PROCESSING.
 RA MEDLINE=20576391; PubMed=11035007;
 RA Pinnix I., Matsuura U., Yun H., Sriharan A., Golde T., Beckman C.,
 RA Ziani-Cherif C., Ostead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative
 RT C-terminal fragment-gamma of amyloid beta protein precursor."
 RT

RL J. Biol. Chem. 276:481-487(2001).

CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.

CC -1- FUNCTION: Apicicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).

CC -1- FUNCTION: The gamma-CRP peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).

CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APB family members, the APPA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FRL1, APPBP1, IBI, KMS2
 CC (via its TPR domains), APPBP2 (via Bass) and DBP1 (By similarity).
 CC Associates with microtubules in the presence of APP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOB in vitro and in vivo. When lipitated,
 CC APOB3 appears to be the preferred amyloid binding isoform, while
 CC the apoB4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Bystn-Alternative splicing: Named isoforms=2:
 CC Comment:Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC apicicans;

CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;

CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP 007221, VSP 007222;

CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.

CC -1- INDUCTION: Increased levels during neuronal differentiation.
 CC -1- DOMAIN: The basolateral sorting signal (Bass) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.

CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of

CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.

CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields p3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTF8).

CC -1- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).

CC -1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the apicicans (By similarity).

CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.

CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).

CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.

CC -1- SIMILARITY: Belongs to the APP family.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----
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 CC or send an email to license@isb.sib.ch).

CC -----

CC EMBL: X97631; CAA66230.1; -
 CC EMBL: X99198; CAA67589.1; -
 CC HSSP: P05067; 1BA4.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRODOM: PD000222; Kunitz_BPTI; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS02279; BPTI_KUNITZ_2; 1.
 CC Apoptosis: Endocytosis; Cell adhesion; Serine protease inhibitor;
 CC Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 CC Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 CC Proteoglycan; Alternative splicing; Amyloid.
 CC SIGNAL 1 17
 CC CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 CC CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
 CC CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
 CC CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
 CC CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 CC CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).

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FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
FT CHAIN 688 713 P3(42) (BY SIMILARITY).
FT CHAIN 688 711 P3(42) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).

Query Match 40.8%; Score 62; DB 1; Length 770;
Best Local Similarity 40.6%; Pred. No. 0.19;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Qy 1 DAEPFRHDSGYEYHOKLVPPEDVGSNGKAI 703
Db 672 DAEPFRHDSGYEYHOKLVPPEDVGSNGKAI 703

RESULT 9
ID A4 HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q8BT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UC58;
DT 13-NOV-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hominidae; Homin.
OX NCBI_TaxID=9606;
(1)
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RT Nature 325:733-736(1987).
(2)
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhite P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proenzyme inhibitors.";
RT Nature 331:525-527(1988).
(3)
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128472; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PrpA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RT Nucleic Acids Res. 17:517-522(1989).
(4)
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90036318; PubMed=2110105;
RA Yoshikata S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RT Gene 87:257-263(1990).
(5)

RP ERRATUM, AND REVISIONS.
RA Yoshikata S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
RT Gene 102:291-292(1991).
(6)
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RT J. Biol. Chem. 267:10804-10809(1992).
(7)
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tanahara R., Furuhata Y., Tanahashi H., Hirose M.,
RA Salto M., Teukuni S., Sasaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RT Nucleic Acids Res. 25:1802-1808(1997).
(8)
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RT Eur. J. Neurosci. 16:102-108(2003).
(9)
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Tsibiyk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gamarate P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
(10)
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon B.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RT Nucleic Acids Res. 16:9351-9351(1988).
(11)
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon B.A.;
RT Nucleic Acids Res. 16:11402-11402(1988).
(12)
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RT Biochem. Biophys. Res. Commun. 159:297-304(1989).
(13)

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RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast; PubMed=3597385;
 RX MEDLINE=87250662; van Nostrand W.E., Cunningham D.D.;
 RA "Purification of protease nexin II from human fibroblasts.";
 RT J. Biol. Chem. 262:8508-8514(1987).
 RL (14)
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RP TISSUE=Brain;
 RC MEDLINE=89346754; PubMed=2569763;
 RX de Sauvage F., Octave J.N.;
 RA "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN (15)
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RL cerebrovascular and the neuritic plaque amyloid peptides.";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RP (16)
 RP SEQUENCE OF 286-366 FROM N.A.;
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.B., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Guealla J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RL mRNA associated with Alzheimer's disease.";
 RN Nature 331:528-530(1988).
 RP (17)
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RL protease inhibitory activity.";
 RN Nature 331:530-532(1988).
 RP (18)
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RL disease brain: coding and noncoding regions of the fetal precursor
 RN mRNA are expressed in the cortex.";
 RP Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RP (19)
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160; Multhaup G.;
 RA Behner D., Heese L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RL mapping of the binding sites on APP and collagen type I.";
 RN J. Biol. Chem. 271:1613-1620(1996).
 RP (20)
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
 RP AND AD GLY-717
 RX MEDLINE=93236601; PubMed=8476439;
 RA Demann R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RL mutations on the processing of the beta-amyloid peptide precursor.";
 RN Biochem. Biophys. Res. Commun. 192:96-103(1993).
 RP (21)
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.B., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RL similarity to soybean trypsin inhibitor.";
 RN Biochem. Biophys. Res. Commun. 163:1246-1255(1989).
 RP (22)
 Query Match 40.8%; Score 62; DB 1; Length 770;

Best Local Similarity 40.6%; Pred. No. 0.19;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
 QY 1 DAEFRDGGYKI-----SITEIKGVIV 22
 DB 672 DAEFRDGGYKVHDKLVPAEDVGSNKALII 703
 RESULT 10
 A4_MACEA STANDARD; PRT; 770 AA.
 ID A4_MACEA
 AC P53601; Q95KN7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DB amyloid protein homolog) (contains: soluble APP-alpha (S-APP-alpha);
 DB Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (beta-
 DB APP42); Beta-amyloid protein 40 (beta-APP40); C83; P3(42); P3(40);
 DB Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DB (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DB secretase C-terminal fragment 50); C31).
 GN APP.
 OS Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey).
 OC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
 RP TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlany M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RL supports a primate model for beta amyloidosis in Alzheimer's
 RN disease.";
 RP Am. J. Pathol. 138:1423-1435(1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tipe60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or its potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, PPRI1, APPBP1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DDN1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated

pite. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).
 -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=APP770;
 IsoId=PS3601-1; Sequence=Displayed;
 Name=APP695;
 IsoId=PS3601-2; Sequence=VSP_000010, VSP_000011;
 -1- DOMAIN: The basolateral sorting signal (bASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).
 -1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).
 -1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptide. S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptide. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/alpha-secretin-mediated gamma-secretase processing of C99 releases the amyloid beta protein, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).
 -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).
 -1- PTM: N- and O-glycosylated (By similarity).
 -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).
 -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).
 Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).
 -1- SIMILARITY: Belongs to the APP family.
 -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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 EMBL: MS8727; AAA36829.1; -
 EMBL: MS8726; AAA36828.1; -
 HSSP: P05067; 1AAP.
 InterPro: IPR008155; A4_APP.
 InterPro: IPR008154; A4_extra.
 InterPro: IPR001255; Beta_APP.
 InterPro: IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4 EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PRINTS; PR00759; BASICPTASE.
 DR Prodom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4 EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4 EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KM Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KM Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
 KM Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KM Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 C83 (POTENTIAL).
 FT CHAIN 688 711 P3(42) (POTENTIAL).
 FT CHAIN 712 770 P3(40) (POTENTIAL).
 FT CHAIN 714 770 GAMMA-CTF(59) (POTENTIAL).
 FT CHAIN 721 770 GAMMA-CTF(57) (POTENTIAL).
 FT CHAIN 740 770 GAMMA-CTF(50) (POTENTIAL).
 FT TRANSMEM 18 699 C31 (POTENTIAL).
 FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 724 770 POTENTIAL.
 FT DOMAIN 96 110 CYTOSOLASMIC (POTENTIAL).
 FT DOMAIN 181 188 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 391 423 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 423 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
 FT SITE 724 734 BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
 FT SITE 739 740 CLEAVAGE (BY CASPASES-3, -6, -8 OR -9)

Query Match 40.8%; Score 62; DB 1; Length 770;
 Best Local Similarity 40.6%; Pred. No. 0.19;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
 1 DAEFRHDSGYVYI-----SITEIKGVIV 22
 Db 672 DAEFRHDSGYVHHQKLVPAEDVGSNKGAIL 703

RESURF 11
ID A4_PIG STANDARD; PRT; 770 AA.
AC P79307; Q29023; Q9TU10;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31).
OS Sue scrofa (Pig).
OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-136 FROM N.A.
RA TISSUE=Small intestine;
RA Winteroe A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine CDNA
RT library.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 667-723 FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris P.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-303(1991).
RN [4]
RP FUNCTION: Functions as a cell surface receptor and performs
RP physiological functions on the surface of neurons relevant to
RP neurite growth, neuronal adhesion and axonogenesis. Involved in
RP cell mobility and transcription regulation through protein-protein
RP interactions (By similarity). Can promote transcription activation
RP through binding to APBB1/Tipeo and inhibit Notch signaling through
RP interaction with Numb (By similarity). Couples to apoptosis-
RP inducing pathways such as those mediated by G(O) and JIP (By
RP similarity). Inhibits G(O) alpha ATPase activity (By similarity).
RP Acts as a kinesin I membrane receptor, mediating the axonal
RP transport of beta-secretase and presenilin 1 (By similarity). May
RP be involved in copper homeostasis/oxidative stress through copper
RP ion reduction (By similarity). In vitro, copper-metalated APP
RP induces neuronal death directly or is potentiated through Cu(II)-
RP mediated low-density lipoprotein oxidation (By similarity). Can
RP regulate neurite outgrowth through binding to components of the
RP extracellular matrix such as heparin and collagen I and IV (By
RP similarity).
RN [5]
RP FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
RP with metal-reducing activity. Bind transient metals such as
RP copper, zinc and iron (By similarity).
RN [6]
RP FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
RP peptides, including C31, are potent enhancers of neuronal
RP apoptosis (By similarity).
RN [7]
RP SUBUNIT: Binds, via its C-terminal, to the PID domain of several
RP cytoplasmic proteins, including APBB family members, the APBA
RP family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
RP to Dab1 inhibits its serine phosphorylation (By similarity). Also
RP interacts with GPCR-like protein BPP, FRIL, APPBP1, IBI, KNS2
RP (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1.
RP In vitro, it binds MAPT via the WT-binding domains (By
RP similarity). Associates with microtubules in the presence of ATP
RP and in a kinesin-dependent manner (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity). (BASS) is required for
CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -1- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields p3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -1- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -1- SIMILARITY: Belongs to the APP family.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC
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CC
CC EMBL: AB032550; BAA84580.1; -
CC EMBL: Z84022; CAB06313.1; -
CC EMBL: X56127; CAA39592.1; -
CC HSSP: P05067; 1AAP.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR002223; Kunitz_BPT1.
CC Pfam: PF02177; A4_EXTRA; 1.
CC PRINTS: PR00203; AMYLOIDA4.

DR PRINTS; PRO0759; BASICPTASE.
 DR ProDom; PDD000222; Kunitz_BPT1; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
 DR Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KM Coated pits; Neutrons; Heparin-binding; Metal-binding; Copper; Iron;
 KM Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KM Amyloid.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT CHAIN 18 687
 FT CHAIN 18 671
 FT CHAIN 672 770
 FT CHAIN 672 713
 FT CHAIN 672 711
 FT CHAIN 688 770
 FT CHAIN 688 713
 FT CHAIN 712 770
 FT CHAIN 714 770
 FT CHAIN 721 770
 FT CHAIN 740 770
 FT CHAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 96 110
 FT DOMAIN 135 155
 FT DOMAIN 181 188
 FT DOMAIN 291 341
 FT DOMAIN 391 423
 FT DOMAIN 491 522
 FT DOMAIN 523 540
 FT DOMAIN 732 751
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT ACT SITE 301 302
 FT SITE 671 672
 FT SITE 672 673
 FT SITE 687 688
 FT SITE 704 704
 FT SITE 706 706
 FT SITE 711 712
 FT SITE 713 714
 FT SITE 720 721

Query Match 40.8%; Score 62; DB 1; Length 770;
 Best Local Similarity 40.8%; Pred. No. 0.19;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

1 DAEFRHDSGYKI-----SITRIKGVIV 22
 DB 672 DAEFRHDSGYEVRHOKLVFPAPADVGSNKGALI 703

RESULT 12
 VGLF_RINDR STANDARD; PRT; 546 AA.
 ID VGLF_RINDR
 AC P41360;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 OS F.
 GN Rinderpest virus (strain RB71) (RDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=39007;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95088609; PubMed=7996154;
 RA Evans S.A., Baron M.D., Chamberlain R.W., Coatsley L., Barrett T.;
 RT "Nucleotide sequence comparisons of the fusion protein gene from
 RT virulent and attenuated strains of rinderpest virus";
 RL J. Gen. Virol. 75:3611-3617(1994).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC
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 CC -----
 CC EMBL; Z31656; CAAB3482.1; -;
 DR PIR; S47300; S47300.
 DR HSSP; P04849; 1SVF.
 DR InterPro; IPR000776; Fusion gly.
 DR Pfam; PF00523; Fusion gly. 1.
 DR Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 546
 FT CHAIN 20 108
 FT CHAIN 109 546
 FT CHAIN 109 108
 FT TRANSMEM 109 133
 FT DOMAIN 109 133
 FT TRANSMEM 484 517
 FT DOMAIN 514 517
 FT DISULFID 64 191
 FT CARBOHYD 25 25
 FT CARBOHYD 57 57
 FT CARBOHYD 63 63
 FT CARBOHYD 518 518
 FT SEQUENCE 546 AA; 58418 MW; 38B539B89344F401 CRC64;

Query Match 40.1%; Score 61; DB 1; Length 546;
 Best Local Similarity 61.1%; Pred. No. 0.19;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

13 SITRIKGVIVRIETILF 30
 DB 283 SLSTRIKGVIVRIETILF 300

RESULT 13
 VGLF_RINDR STANDARD; PRT; 546 AA.
 ID VGLF_RINDR
 AC P41360;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 OS F.
 GN Rinderpest virus (strain RB0X) (RDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.

NCBI_TaxID=36409;
 (1) SEQUENCE FROM N.A.
 MEDLINE=9508609; PubMed=7996154;
 RA Evans S.A., Barton M.D., Chamberlain R.W., Coatsley L., Barrett T.;
 RT "Nucleotide sequence comparisons of the fusion protein gene from
 RT virulent and attenuated strains of rinderpest virus.";
 RL J. Gen. Virol. 75:3611-3617(1994).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC -----
 DR EMBL; Z30700; CAA83186.1; -;
 DR PIR; S47305; S47305.
 DR HSSP; P04849; ISVP.
 DR InterPro; IPR000776; Fusion_gly.
 DR Pfam; PF00523; fusion_gly; 1.
 KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 546
 FT CHAIN 108
 FT DOMAIN 109 546
 FT TRANSMEM 109 133
 FT TRANSMEM 484 513
 FT DOMAIN 514 517
 FT DISULFID 64 191
 FT CARBOHYD 25 25
 FT CARBOHYD 57 57
 FT CARBOHYD 63 63
 FT CARBOHYD 518 518
 SO SEQUENCE 546 AA; 58705 MW; EDD3F8AFDBECB95 CRC64;
 Query Match 39.5%; Score 60; DB 1; Length 546;
 Best Local Similarity 55.6%; Pred. No. 0.27;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 13 SITRIKGVIRIETILP 30
 DB 283 SLSEIKGVIRHLEGVSY 300
 RESULT 14
 VGLP CDVO STANDARD; PRT; 662 AA.
 AC P12569; Q65991;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Canine distemper virus (strain Onderstepoort) (CDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 NCBI_TaxID=11233;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=88129050; PubMed=3433924;
 RA Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
 RT "The nucleotide sequence of the gene encoding the F protein of canine

distemper virus: a comparison of the deduced amino acid sequence with
 other paramyxoviruses.";
 RL Virus Res. 8:373-386(1987).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93227696; PubMed=8470428;
 RA Wild T.F., Bernard A., Spehner D., Villevial D., Drillean R.;
 RT "Vaccination of mice against canine distemper virus-induced
 RT encephalitis with vaccinia virus recombinants encoding measles or
 RT canine distemper virus antigens.";
 RL Vaccine 11:438-444(1993).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC -----
 DR EMBL; M21849; AAA42878.1; -;
 DR EMBL; X65509; CAA6481.1; -;
 DR PIR; J50321; VGNZCD.
 DR PIR; S21382; S21382.
 DR HSSP; P04849; ISVP.
 DR InterPro; IPR000776; Fusion_gly.
 DR Pfam; PF00523; fusion_gly; 1.
 KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 FT SIGNAL 1 1
 FT CHAIN 2 662
 FT CHAIN 224
 FT CHAIN 225
 FT TRANSMEM 606 662
 FT TRANSMEM 307 307
 FT DISULFID 62 62
 FT CARBOHYD 141 141
 FT CARBOHYD 173 173
 FT CARBOHYD 179 179
 FT CONFLICT 3 3
 FT CONFLICT 140 140
 FT CONFLICT 152 152
 FT CONFLICT 171 171
 FT CONFLICT 174 174
 FT CONFLICT 662 662
 SO SEQUENCE 662 AA; 72970 MW; FB2C81C9797805F0 CRC64;
 Query Match 38.8%; Score 59; DB 1; Length 662;
 Best Local Similarity 50.0%; Pred. No. 0.47;
 Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 13 SITRIKGVIRIETILP 30
 DB 399 TLSEVGVIRHLEGVSY 416
 RESULT 15
 VGLP MEASV STANDARD; PRT; 534 AA.
 AC P26032;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Measles virus (strain Yamagata-1) (Subacute sclerosing panencephalitis
 OS virus).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxId=11239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90385702; PubMed=1698327;
RA Komase K., Haga T., Yoshikawa Y., Sato T.A., Yamanouchi K.;
RT Molecular analysis of structural protein genes of the Yamagata-1
RT strain of defective subacute sclerosing panencephalitis virus. IV.
RT Nucleotide sequence of the fusion gene.";
RL Virus Genes 4:173-181(1990).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC -----
DR EMBL: D10548; BAA01405.1; -.
DR HSP: P04849; ISVF.
DR InterPro: IPR00076; Fusion_gly.
DR Pfam: PF00523; fusion_gly; 1.
KM Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 534 FUSION GLYCOPROTEIN F0.
FT CHAIN 24 112 PROTEIN F2.
FT CHAIN 113 534 PROTEIN F1.
FT TRANSMEM 113 136 POTENTIAL.
FT DOMAIN 137 494 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 495 515 POTENTIAL.
FT DOMAIN 516 534 CYTOPLASMIC (POTENTIAL).
FT DISULFID 68 195 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 534 AA; 57963 MW; F5B21757E643844D CRC64;

Query Match 38.2%; Score 58; DB 1; Length 534;
Best Local Similarity 55.6%; Pred. No. 0.53;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVIVHRIETILF 30
DB 287 TLSEIKGVIVHRLGVSY 304

Search completed: June 18, 2004, 19:59:36
Job time : 5.88957 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 29.0798 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294a-71

Perfect score: 152
Sequence: 1 DAEFRHDSGYKSIITIKGVIVRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	42.1	82	4 Q16014	Q16014 homo sapien
2	62	40.8	33	4 Q9UC33	Q9UC33 homo sapien
3	62	40.8	82	4 Q16020	Q16020 homo sapien
4	62	40.8	82	4 Q16019	Q16019 homo sapien
5	62	40.8	113	13 Q8TH58	Q8TH58 chelydra se
6	62	40.8	534	13 Q9J296	Q9J296 gallus galli
7	62	40.8	569	13 Q9PVL1	Q9PVL1 gallus galli
8	62	40.8	695	13 Q9DGJ8	Q9DGJ8 gallus galli
9	62	40.8	751	13 Q9DGJ7	Q9DGJ7 gallus galli
10	61	40.1	19	4 Q9UCD1	Q9UCD1 homo sapien
11	61	40.1	28	4 Q9UCD1	Q9UCD1 homo sapien
12	61	40.1	30	4 Q9UCD9	Q9UCD9 homo sapien
13	61	40.1	546	12 Q9JH45	Q9JH45 rinderpest
14	60	39.5	546	12 Q84926	Q84926 peste-des-p
15	59.5	39.1	552	12 Q66147	Q66147 cetacean mo
16	59	38.8	528	12 Q9YJW9	Q9YJW9 canine diet

17	59	38.8	530	12 Q8QV06	Q8QV06 canine diet
18	59	38.8	662	12 Q9DX22	Q9DX22 canine diet
19	59	38.8	662	12 Q9JKN3	Q9JKN3 canine diet
20	59	38.8	662	12 Q9YKL7	Q9YKL7 canine diet
21	59	38.8	662	12 Q89327	Q89327 canine diet
22	58	38.2	534	12 Q04243	Q04243 measles vir
23	58	38.2	537	12 Q04242	Q04242 measles vir
24	58	38.2	545	12 Q9PXA4	Q9PXA4 measles vir
25	58	38.2	550	12 P90331	P90331 measles vir
26	58	38.2	550	12 Q9QBX0	Q9QBX0 measles vir
27	58	38.2	550	12 Q9QEW9	Q9QEW9 measles vir
28	58	38.2	550	12 P90330	P90330 measles vir
29	58	38.2	550	12 Q9QEW7	Q9QEW7 measles vir
30	58	38.2	550	12 Q9WMT4	Q9WMT4 measles vir
31	58	38.2	550	12 Q89495	Q89495 measles vir
32	58	38.2	550	12 Q8V049	Q8V049 measles vir
33	58	38.2	550	12 Q9YJ94	Q9YJ94 measles vir
34	58	38.2	550	12 Q9QEX1	Q9QEX1 measles vir
35	58	38.2	550	12 Q9QEW8	Q9QEW8 measles vir
36	58	38.2	553	12 Q93055	Q93055 measles vir
37	58	38.2	553	12 Q9IC36	Q9IC36 measles vir
38	58	38.2	553	12 P88973	P88973 measles vir
39	58	38.2	553	12 Q83536	Q83536 measles vir
40	58	38.2	553	12 Q11383	Q11383 measles vir
41	58	38.2	553	12 Q91FK2	Q91FK2 measles vir
42	58	38.2	553	12 Q83533	Q83533 measles vir
43	58	38.2	553	12 Q83525	Q83525 measles vir
44	58	38.2	553	12 Q83518	Q83518 measles vir
45	58	38.2	553	12 P88974	P88974 measles vir

ALIGNMENTS

RESULT 1
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (T-REMBLrel. 01, Created)
DT 01-NOV-1996 (T-REMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-REMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9323601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IKA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; P534AA5B3BA9230A CRC64;

Query Match 42.1%; Score 64; DB 4; Length 82;
Best Local Similarity 34.8%; Pred. No. 0.081;
Matches 16; Conservative 6; Mismatches 8; Indels 16; Gaps 2;

QY 1 DAEFRHDSGYKSIITIKGVIVRIETILF 30
Db 16 DAEFRHDSGYKSIITIKGVIVRIETILF 30
RESULT 2
Q9UC33

```
ID Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seibert F., Vige-Pellrey C., Bach F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlerhurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids."
RL Nature 359:325-327(1992).
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 33 AA; 3674 MW; BIDFE2P4167ABD0 CRC64;

Query Match 40.8%; Score 62; DB 4; Length 33;
Best Local Similarity 40.6%; Pred. No. 0.057;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

OY 1 DAEFRHDSGYEYHOKLVFPADVGSNKGAII 22
Db 1 DAEFRHDSGYEYHOKLVFPADVGSNKGAII 32

RESULT 3
Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON TER 1
FT NON TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5A5E9230A CRC64;

Query Match 40.8%; Score 62; DB 4; Length 82;
Best Local Similarity 40.6%; Pred. No. 0.16;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
```

```
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON TER 1
FT NON TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 40.8%; Score 62; DB 4; Length 82;
Best Local Similarity 40.6%; Pred. No. 0.16;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

OY 1 DAEFRHDSGYEYHOKLVFPADVGSNKGAII 22
Db 18 DAEFRHDSGYEYHOKLVFPADVGSNKGAII 49

RESULT 5
Q8JH58 PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC Testudines; Cryptodira; Testudinidae; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Oxyphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina."
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AA04908.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
FT NON TER 113
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496B053 CRC64;

Query Match 40.8%; Score 62; DB 13; Length 113;
Best Local Similarity 40.6%; Pred. No. 0.23;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;
```

RESULT 6

093296 PRELIMINARY; PRT; 534 AA.
 ID 093296;
 AC 093296;
 DT 01-NOV-1998 (TRMBLrel. 08, Created)
 DT 01-NOV-1998 (TRMBLrel. 08, last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Buteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98337885; PubMed:9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 RT substrate for caspase-3 in dying motoneurons.";
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL: AF042098; AAC25052.1; -
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 534 AA; 60597 MW; FB53EC2B6D4C92 CRC64;

Query Match 40.8%; Score 62; DB 13; Length 534;
 Best Local Similarity 40.6%; Pred. No. 1.4;

Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Qy 1 DAEFRHDSGYKI-----SITEIKGVIV 22
 Db 436 DAEFRHDSGYVHDKLVFPAEDVGSNKGLI 467

RESULT 7

09PVL1 PRELIMINARY; PRT; 569 AA.
 ID 09PVL1;
 AC 09PVL1;
 DT 01-MAY-2000 (TRMBLrel. 13, Created)
 DT 01-MAY-2000 (TRMBLrel. 13, last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Buteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain; Pailga K., Beyreuther K., Masters C.L.;
 RA Coulson E.V.;
 RT "The evolution of the amyloid protein precursor supergene family
 RT tells us about its function.";
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL: AF030441; AAP12698.1; -
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.

DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 40.8%; Score 62; DB 13; Length 569;
 Best Local Similarity 40.6%; Pred. No. 1.5;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Qy 1 DAEFRHDSGYKI-----SITEIKGVIV 22
 Db 472 DAEFRHDSGYVHDKLVFPAEDVGSNKGLI 503

RESULT 8

09DGJ8 PRELIMINARY; PRT; 695 AA.
 ID 09DGJ8;
 AC 09DGJ8;
 DT 01-MAR-2001 (TRMBLrel. 16, Created)
 DT 01-MAR-2001 (TRMBLrel. 16, last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Buteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolase A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289218; AAG00593.1; -
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 40.8%; Score 62; DB 13; Length 695;
 Best Local Similarity 40.6%; Pred. No. 1.9;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Qy 1 DAEFRHDSGYKI-----SITEIKGVIV 22
 Db 597 DAEFRHDSGYVHDKLVFPAEDVGSNKGLI 628

RESULT 9

09DGJ7 PRELIMINARY; PRT; 751 AA.
 ID 09DGJ7;
 AC 09DGJ7;
 DT 01-MAR-2001 (TRMBLrel. 16, Created)
 DT 01-MAR-2001 (TRMBLrel. 16, last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, last annotation update)
 DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Buteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)

RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.:
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms."
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF289219; AAC00594.1; -
 DR HSSP; P05067; IBA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPRASE.
 DR PRODOM; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 DR Protease inhibitor; Serine protease inhibitor.
 KW SEQUENCE 751 AA; 84705 MW; E78E9413A803D84 CRC64;

Query Match 40.8%; Score 62; DB 13; Length 751;
 Best Local Similarity 40.6%; Pred. No. 2;
 Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

OY 1 DAEFRHDSGYKI-----STELKGVIV 22
 DB 653 DAEFRHDSGYRHHOKLVFPAEDVGSNNKGAII 684

RESULT 10
 ID Q9UCB8 PRELIMINARY; PRT; 19 AA.
 AC Q9UCB8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta-amyloid-(1-42) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94068497; PubMed=8248178;
 RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
 RA Gowing E., Ball M.J.;
 RT "beta-amyloid-(1-42) is a major component of cerebrovascular amyloid
 RT deposits: implications for the pathology of Alzheimer disease."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
 DR HSSP; P05067; IAMB.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 SQ SEQUENCE 19 AA; 2315 MW; 05B02B3FEDBCE3B CRC64;

Query Match 40.1%; Score 61; DB 4; Length 19;
 Best Local Similarity 83.3%; Pred. No. 0.043;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYKI 12
 DB 1 DAEFRHDSGYEV 12

RESULT 11

O9UCD1
 ID Q9UCD1 PRELIMINARY; PRT; 28 AA.
 AC Q9UCD1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94045685; PubMed=8229004;
 RA Vligo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
 RT "Characterization of beta-amyloid peptide from human cerebrospinal
 RT fluid."
 RL J. Neurochem. 61:1965-1968(1993).
 DR HSSP; P05067; IAMB.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match 40.1%; Score 61; DB 4; Length 28;
 Best Local Similarity 83.3%; Pred. No. 0.067;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYKI 12
 DB 1 DAEFRHDSGYEV 12

RESULT 12
 ID Q9UCA9 PRELIMINARY; PRT; 30 AA.
 AC Q9UCA9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta-amyloid protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94153015; PubMed=8109908;
 RA Wisniewski T., Lelowski M., Levy B., Marques M.R., Frangione B.;
 RT "The amino acid sequence of neuritic plaque amyloid from a familial
 RT Alzheimer's disease patient."
 RL Ann. Neurol. 35:245-246(1994).
 DR HSSP; P05067; IBA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match 40.1%; Score 61; DB 4; Length 30;
 Best Local Similarity 83.3%; Pred. No. 0.072;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYKI 12
 DB 1 DAEFRHDSGYEV 12

RESULT 13
 ID Q91HA5 PRELIMINARY; PRT; 546 AA.
 AC Q91HA5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

```

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fusion protein.
GN F.
OS Rinderpest virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RX MEDLINE=21014265; PubMed=1186456;
RA Alancot P.K., Smelev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RT "Primary structure of the F-gene from Rinderpest virus strain K.";
RU Mol. Gen. Microbiol. Virusol. 4:29-33(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RA Gusev A.A.;
RA Avancot P.K., Smelev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RU Submitted (May-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL, AY035887; AAK63190.1; -.
DR PIR, P00866; P00866.
DR PIR, P00867; P00867.
DR PIR, P00873; P00873.
DR GO, GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO, GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro, IPR000776; Fusion_gly; I.
DR Pfam, PF00523; fusion_gly; I.
SQ SEQUENCE 546 AA; 58572 MW; 449B2B2DD7405F08 CRC64;

Query Match 40.1%; Score 61; DB 12; Length 546;
Best Local Similarity 61.1%; Pred. No. 2;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
DB 283 TLSIKGVVHRIETILF 300

RESULT 14
Q084926 PRELIMINARY; PRT; 546 AA.
AC 084926;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Peste-des-petites-ruminants virus (PPRV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=31604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VACCINE STRAIN;
RX MEDLINE=96082318; PubMed=7483819;
RA Meyer G., Diello A.;
RT "The nucleotide sequence of fusion protein gene of the Peste des
RT petits ruminants virus: the long untranslated region in the 5' end of
RT the F gene of morbilliviruses seems to be specific to each virus.";
RU Virus Res. 37:23-35(1995).
DR EMBL, Z37017; CA845451.1; -.
DR PIR, S55386; S55386.
DR HSP, P04849; ISVF.
DR GO, GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO, GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro, IPR000776; Fusion_gly.
DR Pfam, PF00523; fusion_gly; I.
SQ SEQUENCE 546 AA; 59310 MW; D77D903A4048A0EB CRC64;

Query Match 39.5%; Score 60; DB 12; Length 546;
Best Local Similarity 61.1%; Pred. No. 2.8;

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Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 13 SITEIKGVVHRIETILF 30
DB 283 TLSIKGVVHRIETILF 300

RESULT 15
Q06147 PRELIMINARY; PRT; 552 AA.
AC 06147;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fusion protein precursor.
OS Cetacean morbillivirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=36410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=porpoise;
RX MEDLINE=95159670; PubMed=7531923;
RA Bolt G.G.B., Blixenkron-Moeller M.M.B., Gottschalk E., Wishaup R.G.,
RA Welsch M.J., Barle J.A.P., Rima B.K.;
RT "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT porpoise and a dolphin.";
RU Virus Res. 34:291-304(1994).
DR EMBL, X80757; CA56731.1; -.
DR PIR, S47034; S47034.
DR HSP, P04849; ISVF.
DR GO, GO:0019039; P:Viral-cell fusion molecule activity; IEA.
DR GO, GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro, IPR000776; Fusion_gly.
DR Pfam, PF00523; fusion_gly; I.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 552 AA; 60025 MW; 40D9191AD910EABE CRC64;

Query Match 39.1%; Score 59.5; DB 12; Length 552;
Best Local Similarity 41.4%; Pred. No. 3.4;
Matches 12; Conservative 7; Mismatches 3; Indels 7; Gaps 1;

QY 9 GYKI-----SITEIKGVVHRIETILF 30
DB 278 GFIVLSIAYPTLSEKGVVHRIETILF 306

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Search completed: June 18, 2004, 20:02:28
Job time : 29.0798 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 46.135 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294a-72
Perfect score: 161
Sequence: 1 DAEPHDSGVKXISTRIKGVYRIETLP 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A GeneSeq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	32	6	AAE35678 Human Ape
2	150	93.2	34	6	AAE35679 Human Ape
3	143	88.8	48	6	AAE35680 Human Ape
4	141	87.6	30	6	AAE35677 Human Ape
5	136	84.5	34	6	AAE35681 Human Ape
6	129	80.1	34	6	AAE35682 Human Ape
7	90	55.9	19	6	AAE35657 Measles v
8	90	55.9	31	7	ADD89946 CD4 pepit
9	90	55.9	45	7	ADD89951 IGE pepit
10	90	55.9	50	7	ADD89944 CD4 pepit
11	87	54.0	65	7	ADD89953 Foot-and-
12	83	51.6	65	7	ADD89952 Foot-and-
13	83	49.7	29	3	AAE35682 Human Ape
14	80	49.7	60	3	AAE35678 Human Ape
15	79	49.1	29	3	AAE35677 Human Ape
16	77	47.8	30	3	AAE35681 Human Ape
17	76	47.2	19	3	AAE35682 Human Ape
18	76	47.2	19	3	AAE35681 Human Ape
19	76	47.2	19	5	ABG68202 Measles v
20	76	47.2	19	5	ABG68208 Measles v
21	76	47.2	19	6	AAE35653 Measles v
22	76	47.2	19	6	AAE35647 Measles v
23	76	47.2	19	6	AAE35644 Measles v
24	76	47.2	29	3	AAE35682 Human Ape
25	76	47.2	29	3	AAE35681 Human Ape

26	76	47.2	30	5	ABG68233 Optimised
27	76	47.2	31	3	AAE35678 Human Ape
28	76	47.2	31	3	AAE35679 Human Ape
29	76	47.2	31	3	AAE35680 Human Ape
30	76	47.2	32	5	ABG68235 Optimised
31	76	47.2	34	5	ABG68231 Optimised
32	76	47.2	35	3	AAE35682 Human Ape
33	76	47.2	36	3	AAE35681 Human Ape
34	76	47.2	36	3	AAE35682 Human Ape
35	76	47.2	36	3	AAE35681 Human Ape
36	76	47.2	39	5	ABG68237 Optimised
37	76	47.2	46	3	AAE35678 Human Ape
38	76	47.2	46	3	AAE35679 Human Ape
39	76	47.2	46	3	AAE35680 Human Ape
40	76	47.2	46	3	AAE35681 Human Ape
41	76	47.2	46	5	ABG68229 Optimised
42	76	47.2	46	5	ABG68227 Optimised
43	76	47.2	47	3	AAE35683 Peptide 1
44	76	47.2	47	3	AAE35680 Human Ape
45	76	47.2	49	3	AAE35678 Human Ape

ALIGNMENTS

RESULT 1	AAE35678	AAE35678 standard, peptide; 32 AA.
ID	AAE35678	
XX	AAE35678;	
AC	23-OCT-2003 (revised)	
XX	17-JUN-2003 (first entry)	
DT	23-OCT-2003 (revised)	
DT	17-JUN-2003 (first entry)	
XX	Human A beta peptide-measles virus Th epitope fusion peptide immunogen #2.	
XX	Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;	
KW	Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;	
KW	vaccine; neurotropic; human; hepatitis B virus; HBV; fusion peptide.	
XX	Homo sapiens.	
OS	Measles virus.	
OS	Chimeric.	
XX	Key	Location/Qualifiers
FT	Region	1..12 "Human beta amyloid peptide"
FT	Region	16..32
FT	Region	/note= "Measles virus T helper cell epitope"
XX	MO200296350-A2.	
XX	05-DEC-2002.	
PD	02-APR-2002; 2002WO-US010293.	
XX	25-MAY-2001; 2001US-00865294.	
XX	(UNBI-) UNITED BIOMEDICAL INC.	
XX	Wang CY;	
XX	WPI; 2003-201258/19.	
DR	Novel peptide immunogen comprising a helper T cell epitope, an N-terminal	
XX	fragment of amyloid beta peptide linked to the epitope, and optionally a	
XX	spacer, useful for preventing or treating Alzheimer's disease.	
XX	Claim 9; Page 39; 77pp; English.	
CC	The present invention relates to a novel peptide immunogen comprising a	
CC	helper T cell (Th) epitope, an N-terminal fragment of amyloid beta	
CC	(Abeta) peptide (residues 1-42) linked to the epitope and optionally a	

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of the
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX XX Sequence 32 AA;

Query Match 100.0%; Score 161; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYVKISITIKGYIVHRIETILF 32
DB 1 DAEFRHDSGYVKISITIKGYIVHRIETILF 32

RESULT 2

AAE35679
ID AAE35679 standard; peptide; 34 AA.

XX AC AAE35679;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
XX Measles virus.
XX OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..14
FT /note= "Human beta amyloid peptide"

FT Region 18..34
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX PD 02-APR-2002; 2002MO-US010293.

XX PR 25-MAY-2001; 2001US-00865294.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
XX fragment of amyloid beta peptide linked to the epitope, and optionally a
XX spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a

CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of the
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX XX Sequence 34 AA;

Query Match 93.2%; Score 150; DB 6; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.3e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEV-KISITIKGYIVHRIETILF 32
DB 1 DAEFRHDSGYEVHKKISITIKGYIVHRIETILF 34

RESULT 3
AAE35680
ID AAE35680 standard; peptide; 48 AA.

XX AC AAE35680;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
XX Measles virus.
XX OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..28
FT /note= "Human beta amyloid peptide"

FT Region 32..48
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX PD 05-DEC-2002.

XX PP 02-APR-2002; 2002MO-US010293.

XX PR 25-MAY-2001; 2001US-00865294.

XX PA (UNBI-) UNITED BIOMEDICAL INC.

XX PI Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
XX fragment of amyloid beta peptide linked to the epitope, and optionally a
XX spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SO Sequence 48 AA;

Query Match 88.8%; Score 143; DB 6; Length 48;
Best Local Similarity 66.7%; Pred. No. 6.5e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

OY 1 DAEFRHDSGYV-----KISTEIKGVIVHRIETILF 32
DB 1 DAEFRHDSGYVHQLVFPADVDGNSNKKISTEIKGVIVHRIETILF 48

RESULT 4

AAE35677
ID AAE35677 standard; peptide; 30 AA.

AC AAE35677;

XX 23-OCT-2003 (revised)

DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.

KM Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;

KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;

XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

OS Homo sapiens.

OS Measles virus.

OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..10 /note= "Human beta amyloid peptide"

FT Region 14..30 /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

XX PS Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

SO Sequence 30 AA;

Query Match 87.6%; Score 141; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 7.2e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYV-----KISTEIKGVIVHRIETILF 32
DB 1 DAEFRHDSGYV-----KISTEIKGVIVHRIETILF 30

RESULT 5

AAE35681
ID AAE35681 standard; peptide; 34 AA.

AC AAE35681;

XX 23-OCT-2003 (revised)

DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.

KM Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;

KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;

XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

OS Homo sapiens.

OS Measles virus.

OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..14 /note= "Human beta amyloid peptide"

FT Region 18..34 /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PT fragment of amyloid beta peptide linked to the epitope, and optionally a
 PT spacer, useful for preventing or treating Alzheimer's disease.
 XX
 PS Disclosure: Page 39; 77pp; English.

CC The present invention relates to a novel peptide immunogen comprising a
 CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
 CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
 CC spacer consisting of at least an amino acid to separate the immunogenic
 CC domains. Sequences of the invention are useful for preventing or treating
 CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
 CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
 CC plaques formed from it. They are useful for eliciting a site-directed
 CC mutagenesis against the main functional/regulatory site of the Abeta
 CC peptide and for generating antibodies, which are highly cross-reactive to
 CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
 CC Alzheimer's disease patients. The sequences are useful for induction of
 CC accelerated clearance of amyloid plaques and immunoneutralisation of the
 CC soluble Abeta derived toxins in the brain to prevent and treat
 CC Alzheimer's disease. They are also useful as vaccines. The present
 CC sequence is human Abeta peptide-measles virus T helper cell epitope.
 CC fusion peptide immunogen used in the exemplification of the invention.
 CC (Updated on 23-Oct-2003 to standardise OS field)

CC
 XX Sequence 34 AA;

Query Match 84.5%; Score 136; DB 6; Length 34;
 Best Local Similarity 85.3%; Pred. No. 5.2e-14;
 Matches 29; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEV--KISITIKGVVHRIETILF 32
 1 DAEFRHDSGYEVHMKISITIKGVVHRIETILF 34

DB 1 DAEFRHDSGYEVHMKISITIKGVVHRIETILF 34
 RESULT 6
 AAB35682
 ID AAB35682 standard; peptide; 34 AA.

AC AAB35682;
 XX
 DT 23-OCT-2003 (revised)
 DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
 KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
 KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
 OS Measles virus.
 OS Chimeric.

XX Key Location/Qualifiers
 FH 1. 14
 FT /note= "Human beta amyloid peptide"
 FT 18. 34
 FT Region /note= "Measles virus T helper cell epitope"

XX MO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
 PT fragment of amyloid beta peptide linked to the epitope, and optionally a
 PT spacer, useful for preventing or treating Alzheimer's disease.
 XX
 PS Disclosure: Page 39; 77pp; English.

CC The present invention relates to a novel peptide immunogen comprising a
 CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
 CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
 CC spacer consisting of at least an amino acid to separate the immunogenic
 CC domains. Sequences of the invention are useful for preventing or treating
 CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
 CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
 CC plaques formed from it. They are useful for eliciting a site-directed
 CC mutagenesis against the main functional/regulatory site of the Abeta
 CC peptide and for generating antibodies, which are highly cross-reactive to
 CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
 CC Alzheimer's disease patients. The sequences are useful for induction of
 CC accelerated clearance of amyloid plaques and immunoneutralisation of the
 CC soluble Abeta derived toxins in the brain to prevent and treat
 CC Alzheimer's disease. They are also useful as vaccines. The present
 CC sequence is human Abeta peptide-measles virus T helper cell epitope.
 CC fusion peptide immunogen used in the exemplification of the invention.
 CC (Updated on 23-Oct-2003 to standardise OS field)

CC
 XX Sequence 34 AA;

Query Match 80.1%; Score 129; DB 6; Length 34;
 Best Local Similarity 85.3%; Pred. No. 6.6e-13;
 Matches 29; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEV--KISITIKGVVHRIETILF 32
 1 DAEFRHDSGYEVHMKISITIKGVVHRIETILF 34

DB 1 DAEFRHDSGYEVHMKISITIKGVVHRIETILF 34
 RESULT 7
 AAE35657
 ID AAE35657 standard; peptide; 19 AA.

AC AAE35657;
 XX
 DT 17-JUN-2003 (first entry)

XX Measles virus T helper cell epitope #31.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
 KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
 KW vaccine; nootropic.

XX Measles virus.
 OS Measles virus.
 OS WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
 PT fragment of amyloid beta peptide linked to the epitope, and optionally a
 PT spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 1; Page 37; 77pp; English.

CC The present invention relates to a novel peptide immunogen comprising a
 CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
 CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
 CC spacer consisting of at least an amino acid to separate the immunogenic
 CC domains. Sequences of the invention are useful for preventing or treating
 CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
 CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
 CC plaques formed from it. They are useful for eliciting a site-directed
 CC immunogens against the main functional/regulatory site of the Abeta
 CC peptide and for generating antibodies, which are highly cross-reactive to
 CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
 CC Alzheimer's disease patients. The sequences are useful for induction of
 CC accelerated clearance of amyloid plaques and immunoneutralisation of the
 CC soluble Abeta derived toxins in the brain to prevent and treat
 CC Alzheimer's disease. They are also useful as vaccines. The present
 CC sequence is measles virus T helper (Th) cell epitope used in the
 CC exemplification of the invention
 CC
 CC Sequence 19 Ab:
 CC
 CC

Query Match	55.9%	Score	90	DB	6	Length	19
Best Local Similarity	100.0%	Pred. No.	4.3e-07				
Matches	19	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

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Qy      14 ISITBIKGVIVHRIETILF 32
        |||||
Db      1 ISITBIKGVIVHRIETILF 19
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RESULT 8
ADD89946
ID ADD89946 standard; protein; 31 AA

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AC	ADD89946;
XX	
DT	29-JAN-2004 (first entry)

DB CD4 peptide used in immunostimulant complex for anti-HIV vaccine.

KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4

OS Synthetic.
OS Homo sapiens.

	Key	location/Qualifiers
FH	Modified-site	20
PT		/note= "Epsilon-lysine"
PT		

PN W02003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

XX

PA (UNBI-) UNITED BIOMEDICAL, INC.

PI Sokol1 KK;

DR WPI: 2003-778890/73.

PT Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.

PS Claim 14; SEQ ID NO 6; 159pp; English.

The present sequence is that of a synthetic immunogenic peptide derived from human CD4. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen

CC stabilised. The complexes comprise a CpG oligonucleotide and a
 CC biologically active peptide immunogen. The complex is particulate and can
 CC efficiently present peptide immunogens to the cells of the immune system
 CC to produce an immune response. The complexes may be prepared with various
 CC ratios of peptides to CpG oligonucleotides to provide different physical
 CC properties, such as the size of the microparticle. An immunostimulatory
 CC complex comprising the present CD4 derived peptide can be used in an anti-
 CC CD4 immunotherapeutic vaccine for the treatment of HIV infection.
 XX
 Sequence 31 AA;

Sequence 31 AA

Query Match	55.9%	Score 90	DB 7	Length 31
Best Local Similarity	100.0%	Pred. No.	8,2e-07	
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY 14 SITEIKGVIWHRIITLF 32
    |||||
Db 1 SITEIKGVIWHRIITLF 19
```

RESULT 9
ADD89951
ID ADD89951 standard; protein: 45 AA

AC	ADD89951;
XX	
DT	29-JAN-2004 (first entry)

DB IGB peptide used in immunostimulant complex for allergy vaccine.

KW Immunostimulant; vaccine; human; immunogen; IgG; immunotherapy; allergy
KW antibody; antiallergic.

OS	Synthetic.
OS	Homo sapiens.

PH	Key	Location/Qualifiers
FT	Modified-site	20
FT		/note= "Epsilon-lysine"

PN W02003068169-A2

PD 21-AUG-2003

PP 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

XX

PA (UNBI -) UNITED BIOMEDICAL INC.

PI Sokol1 KK;

DR WPI: 2003-778890/73.

PT Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.

PS Claim 20; SEQ ID NO 11; 159pp; English.

The present sequence is that of a synthetic immunogenic peptide derived from human IgG. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen stabiliser. The complexes comprise a Cpg oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogens to the cells of the immune system to produce an immune response. The complexes may be prepared with various ratios of peptides to Cpg oligonucleotides to provide different physical properties, such as the size of the microparticle. An immunostimulatory complex comprising the present IgG derived peptide can be used in an anti-IgG immunotherapeutic vaccine for the treatment of allergy.

```

XX      XX      Sequence 45 AA;
SQ      Query Match      55.9%; Score 90; DB 7; Length 45;
      Best Local Similarity 100.0%; Pred. No. 1.3e-06;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      14 ISTEIKGVIVHRIETILF 32
      1 ISTEIKGVIVHRIETILF 19
DB      1 ISTEIKGVIVHRIETILF 19

RESULT 10
ADD89944
ID      ADD89944 standard; protein; 50 AA.
XX
XX      AC      ADD89944;
XX      DT      29-JAN-2004 (first entry)
XX
XX      CD4 peptide used in immunostimulant complex as anti-HIV vaccine.
XX
XX      Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
XX      Synthetic.
XX      OS      Homo sapiens.
XX      Key      Location/Qualifiers
XX      Modified-site 20
XX      /note= "Epsilon-lysine"
XX
XX      WO2003068169-A2.
XX
XX      21-AUG-2003.
XX
XX      14-FEB-2003; 2003WO-US004711.
XX
XX      14-FEB-2002; 2002US-00076674.
XX      PR      31-JAN-2003; 2003US-00076674.
XX
XX      (UNBI-) UNITED BIOMEDICAL INC.
XX
XX      Sokoll KK;
XX
XX      WPI; 2003-778890/73.
XX
XX      Stabilized immunostimulating complex, useful for vaccination, e.g.
XX      against human immune deficiency viruses, comprises cationic peptide
XX      immunogen and anionic oligonucleotide.
XX
XX      Claim 14; SEQ ID NO 4; 159pp; English.
XX
XX      The present sequence is that of a synthetic immunogenic peptide derived
XX      from human CD4. This is an example of peptides that can be used in
XX      claimed immunostimulatory complexes of the invention that are
XX      specifically adapted to act as adjuvant and as peptide immunogen
XX      stabiliser. The complexes comprise a Cpg oligonucleotide and a
XX      biologically active peptide immunogen. The complex is particulate and can
XX      efficiently present peptide immunogens to the cells of the immune system
XX      to produce an immune response. The complexes may be prepared with various
XX      ratios of peptides to Cpg oligonucleotides to provide different physical
XX      properties, such as the size of the microparticle. An immunostimulatory
XX      complex comprising the present CD4 derived peptide can be used in an anti
XX      -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
XX      Sequence 50 AA;
SQ      Query Match      55.9%; Score 90; DB 7; Length 50;
      Best Local Similarity 100.0%; Pred. No. 1.5e-06;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      14 ISTEIKGVIVHRIETILF 32
      1 ISTEIKGVIVHRIETILF 19

```

```

DB      1 ISTEIKGVIVHRIETILF 19

RESULT 11
ADD89953
ID      ADD89953 standard; protein; 65 AA.
XX
XX      AC      ADD89953;
XX      DT      29-JAN-2004 (first entry)
XX
XX      Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
XX      Immunostimulant; vaccine; immunogen; immunotherapy;
XX      foot-and-mouth disease.
XX
XX      Synthetic.
XX      OS      Foot-and-mouth disease virus.
XX      Key      Location/Qualifiers
XX      Modified-site 20
XX      /note= "Epsilon-lysine"
XX
XX      WO2003068169-A2.
XX
XX      21-AUG-2003.
XX
XX      14-FEB-2003; 2003WO-US004711.
XX
XX      14-FEB-2002; 2002US-00076674.
XX      PR      31-JAN-2003; 2003US-00076674.
XX
XX      (UNBI-) UNITED BIOMEDICAL INC.
XX
XX      Sokoll KK;
XX
XX      WPI; 2003-778890/73.
XX
XX      Stabilized immunostimulating complex, useful for vaccination, e.g.
XX      against human immune deficiency viruses, comprises cationic peptide
XX      immunogen and anionic oligonucleotide.
XX
XX      Claim 22; SEQ ID NO 13; 159pp; English.
XX
XX      The present sequence is that of a synthetic immunogenic peptide derived
XX      from foot-and-mouth disease (FMD) virus. This is an example of peptides
XX      that can be used in claimed immunostimulatory complexes of the invention
XX      that are specifically adapted to act as adjuvant and as peptide immunogen
XX      stabiliser. The complexes comprise a Cpg oligonucleotide and a
XX      biologically active peptide immunogen. The complex is particulate and can
XX      efficiently present peptide immunogens to the cells of the immune system
XX      to produce an immune response. The complexes may be prepared with various
XX      ratios of peptides to Cpg oligonucleotides to provide different physical
XX      properties, such as the size of the microparticle. An immunostimulatory
XX      complex comprising the present FMD virus derived peptide can be used in
XX      an anti-FMD vaccine for protective immunity against FMD.
XX
XX      Sequence 65 AA;
SQ      Query Match      54.0%; Score 87; DB 7; Length 65;
      Best Local Similarity 94.7%; Pred. No. 6.5e-06;
      Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      14 ISTEIKGVIVHRIETILF 32
      1 ISTEIKGVIVHRIETILF 19
DB      1 ISTEIKGVIVHRIETILF 19

RESULT 12
ADD89952
ID      ADD89952 standard; protein; 65 AA.
XX
XX      AC      ADD89952;

```

XX 29-JAN-2004 (first entry)
XX Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX Immunostimulant; vaccine; immunogen; immunotherapy;
XX foot-and-mouth disease.
XX Synthetic.
OS Foot-and-mouth disease virus.
OS
XX Key Location/Qualifiers
XX Modified-site 20
XX /note= "Epsilon-lysine"
XX MO2003068169-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003MO-US004711.
XX
XX 14-FEB-2002; 2002US-00076674.
XX 31-JAN-2003; 2003US-00076674.
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Sokoll KK;
XX
XX WPI; 2003-778890/73.
XX
XX Stabilized immunostimulating complex, useful for vaccination, e.g.
XX against human immunodeficiency viruses, comprises cationic peptide
XX immunogen and anionic oligonucleotide.
XX
XX Claim 22; SEQ ID NO 12; 159pp; English.
XX
XX The present sequence is that of a synthetic immunogenic peptide derived
XX from foot-and-mouth disease (FMD) virus. This is an example of peptides
XX that can be used in claimed immunostimulatory complexes of the invention
XX that are specifically adapted to act as adjuvant and as peptide immunogen
XX stabilizer. The complexes comprise a CpG oligonucleotide and a
XX biologically active peptide immunogen. The complex is particularly and can
XX efficiently present peptide immunogens to the cells of the immune system
XX to produce an immune response. The complexes may be prepared with various
XX ratios of peptides to CpG oligonucleotides to provide different physical
XX properties, such as the size of the microparticle. An immunostimulatory
XX complex comprising the present FMD virus derived peptide can be used in
XX an anti-FMD vaccine for protective immunity against FMD.
XX
XX Sequence 65 AA:
XX
XX Query Match 51.6%; Score 83; DB 7; Length 65;
XX Best Local Similarity 89.5%; Pred. NO. 2.8e-05;
XX Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 14 ISITRIKGVVHRIETILP 32
XX |||:|||||:|||||
XX 1 ISISIKGVIVHRIETILP 19
XX
XX RESULT 13
XX ID AAY91264 standard; peptide; 29 AA.
XX
XX AAY91264;
XX
XX 12-SEP-2003 (revised)
XX 22-MAY-2000 (first entry)
XX
XX Modified MWP Th epitope/HIV epitope. SEQ ID NO:142.
XX
XX Promiscuous T-cell epitope; measles virus F protein; MWP;
XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CTRP;
KW cholesterol ester transport protein; anti-arteriosclerotic.
XX
XX Measles virus.
OS Human immunodeficiency virus 1.
OS Chimeric.
XX
XX MO9966957-A2.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99MO-US013975.
XX
XX 20-JUN-1998; 98US-00100412.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX Wang CY;
XX
XX WPI; 2000-160564/14.
XX
XX New artificial T helper cell epitope and derived immunogens with target
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus.
XX
XX Claim 13; Page 63; 129pp; English.
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th)
XX and immunogenic peptides comprising the Th epitopes of the invention
XX along with B cell epitopes. The Th epitopes and peptide immunogens
XX containing them, are used to induce a T helper cell response,
XX specifically against Plasmodium falciparum, cholesterol ester transport
XX protein (CTRP) or HIV epitopes, but more generally against any pathogen,
XX immunoreactive self-antigen or tumour antigen. The Th epitopes and
XX peptide immunogens may be used for prevention and/or treatment of
XX infections (HIV, foot-and-mouth disease or malaria); for cancer
XX immunotherapy; for inhibition of the action of luteinising hormone
XX releasing hormone (LHRH) for contraception, treatment of hormone-
XX dependent cancer, prevention of boar taint in meat, and immunocastration)
XX ; for promoting the growth of animals; or for treating allergies or
XX arteriosclerosis. Incorporation of a promiscuous Th (functional in
XX genetically diverse subjects) into an immunogen improves capacity to
XX induce a strong T helper cell-mediated immune response, resulting in
XX production of antibodies against a target antigen. Th can replace carrier
XX proteins and pathogen-derived T helper epitopes. Sequence AAY91121
XX represents a promiscuous T helper epitope from the measles virus F (MVF)
XX protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
XX represent synthetic Th epitopes based on the MVF Th epitope. Sequence
XX AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
XX surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
XX derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
XX Y91244 are antigenic peptides comprising an LHRH sequence joined to a
XX promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
XX used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
XX AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
XX epitope. Somatostatin immunogens may be used to promote growth in
XX livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
XX AAY91209-Y90211 are MWP Th epitope/CD4 CDR2 antigenic peptides which may
XX be used to prevent HIV infection of T cells. AAY90212 is a modified
XX version of a human IGE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
XX are Th epitope/IGE CH3 antigenic peptides which may be used in the
XX treatment of allergies. AAY91220 is a peptide derived from foot and mouth
XX disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
XX peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
XX circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
XX antigen and an MWP Th epitope and may be used in a malaria vaccine.
XX AAY91228-Y91231 represent CTRP-derived peptides and AAY91232-Y91241 are
XX immunogens comprising a CTRP peptide and a Th epitope which may be used
XX to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
XX and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-

CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVA Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasion protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 29 AA;

Query Match 49.7%; Score 80; DB 3; Length 29;

Best Local Similarity 70.8%; Pred. NO. 2.8e-05;

Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GYEVKISTEIKGVIVHRIETILF 32
| : |||:|||||:| : |||
Db 6 GPGTGISISIKGVIVHRIEGLIF 29

RESULT 14

AAV80078
ID AAY80078 standard; peptide: 60 AA.

AC AAY80078;

DT 15-MAY-2000 (first entry)

DE IGB immunogenic peptide conjugate SEQ ID NO:85.

KM Immunoglobulin E; IGB; epsilon heavy chain; antigenic; antigen;
KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KM antibody; allergy; allergic disease; immunisation; anti-allergic;
KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Unidentified.

OS

PN MO9967293-A1.

PD 29-DEC-1999.

PP 21-JUN-1999; 99WO-US013959.

PR 20-JUN-1998; 98US-00100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfeld AM;

DR WPI; 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

PT for immunization against allergy.

PS Claim 14; Page 76; 155pp; English.

XX The present invention describes immunoglobulin E (IGB)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IGB, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IGB synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IGB-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX Sequence 60 AA;

Query Match 49.7%; Score 80; DB 3; Length 60;
Best Local Similarity 75.0%; Pred. NO. 7.4e-05;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GYEVKISTEIKGVIVHRIETILF 32
| : |||:|||||:| : |||
Db 10 GKEGGISISIKGVIVHRIEGLIF 33

RESULT 15

AAV91266
ID AAY91266 standard; peptide: 29 AA.

AC AAY91266;

DT 12-SEP-2003 (revised)

DT 22-MAY-2000 (first entry)

DE Modified MVA Th epitope/HIV epitope, SEQ ID NO:144.

KM Promiscuous T-cell epitope; measles virus F protein; MVA;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
KM foot and mouth disease virus; immunoglobulin E; IGB; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KM cholesterol ester transport protein; anti-arteriosclerotic.

OS Measles virus.

OS Human immunodeficiency virus 1.

OS Chimeric.

PN MO996957-A2.

PD 29-DEC-1999.

PP 21-JUN-1999; 99WO-US013975.

PR 20-JUN-1998; 98US-00100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target

PT antigenic site, for immunization against e.g. malaria, arteriosclerosis

PT or human immune deficiency virus.

PS Claim 13; Page 63; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 12.5644 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-72

Perfect score: 161
Sequence: 1 DABFRHDSGVKISITKGVVIRITLIF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	47.2	19	3	US-09-100-414B-15
2	76	47.2	19	3	US-09-303-323-15
3	76	47.2	19	4	US-09-770-014-15
4	76	47.2	31	3	US-09-100-414B-53
5	76	47.2	31	3	US-09-303-323-53
6	76	47.2	31	4	US-09-770-014-53
7	76	47.2	35	3	US-09-100-414B-80
8	76	47.2	35	3	US-09-303-323-80
9	76	47.2	35	4	US-09-770-014-80
10	76	47.2	46	3	US-09-100-414B-96
11	76	47.2	46	3	US-09-303-323-96
12	76	47.2	46	4	US-09-770-014-96
13	76	47.2	47	3	US-09-100-414B-60
14	76	47.2	47	4	US-09-303-323-60
15	76	47.2	47	3	US-09-770-014-60
16	76	47.2	49	3	US-09-100-414B-57
17	76	47.2	49	3	US-09-303-323-57
18	76	47.2	49	4	US-09-770-014-57
19	76	47.2	80	3	US-09-100-600A-30
20	72.5	45.0	35	2	US-08-612-785B-15
21	72.5	45.0	35	4	US-08-612-785C-15
22	71.5	44.4	35	2	US-08-612-785B-39
23	71	44.1	19	3	US-09-100-414B-17
24	71	44.1	19	3	US-09-303-323-17
25	71	44.1	19	4	US-09-770-014-17
26	71	44.1	31	3	US-09-100-414B-55
27	71	44.1	31	3	US-09-303-323-55

28	71	44.1	31	4	US-09-770-014-55	Sequence 55, Appl
29	69	42.9	19	3	US-09-100-414B-18	Sequence 18, Appl
30	69	42.9	19	3	US-09-100-414B-19	Sequence 19, Appl
31	69	42.9	19	3	US-09-100-414B-20	Sequence 20, Appl
32	69	42.9	19	3	US-09-303-323-18	Sequence 18, Appl
33	69	42.9	19	3	US-09-303-323-19	Sequence 19, Appl
34	69	42.9	19	4	US-09-303-323-20	Sequence 20, Appl
35	69	42.9	19	4	US-09-770-014-18	Sequence 18, Appl
36	69	42.9	19	4	US-09-770-014-19	Sequence 19, Appl
37	69	42.9	19	4	US-09-770-014-20	Sequence 20, Appl
38	69	42.9	31	3	US-09-100-414B-56	Sequence 56, Appl
39	69	42.9	31	3	US-09-100-414B-59	Sequence 59, Appl
40	69	42.9	31	3	US-09-100-414B-61	Sequence 61, Appl
41	69	42.9	31	3	US-09-303-323-56	Sequence 56, Appl
42	69	42.9	31	3	US-09-303-323-59	Sequence 59, Appl
43	69	42.9	31	3	US-09-303-323-61	Sequence 61, Appl
44	69	42.9	31	4	US-09-770-014-56	Sequence 56, Appl
45	69	42.9	31	4	US-09-770-014-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-15
Sequence 15, Application US/09100414B
Patent No. 6025468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: peptide

US-09-100-414B-15

Query Match 47.2% Score 76; DB 3; Length 19;

Best Local Similarity 84.2% Pred. No. 1e-05; Indexes 0; Gaps 0;

Matches 16; Conservative 2; Mismatches 1; Indels 0;

Oy 14 ISITKGVVIRITLIF 32

Db 1 ISITKGVVIRITLIF 19

RESULT 2

US-09-303-323-15
Sequence 15, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-15

Query Match 47.2% Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 ISITEIKGVIYRIETILF 32
|||:|||||||:|||||
DB 1 ISITEIKGVIYRIETILF 19

RESULT 3
US-09-770-014-15
Sequence 15, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-15

Query Match 47.2% Score 76; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 ISITEIKGVIYRIETILF 32
|||:|||||||:|||||
DB 1 ISITEIKGVIYRIETILF 19

RESULT 4
US-09-100-414B-53
Sequence 53, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-53

Query Match 47.2% Score 76; DB 3; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.9e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVHRIETILF 32
DB 1 ISISEIKGVIVHRIEGLF 19

RESULT 5

US-09-303-323-53
; Sequence 53, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; US-09-303-323-53

Query Match 47.2%; Score 76; DB 3; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.9e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVHRIETILF 32
DB 1 ISISEIKGVIVHRIEGLF 19

RESULT 6

US-09-770-014-53
; Sequence 53, Application US/09770014
; Patent No. 6559282
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA

ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; US-09-770-014-53

Query Match 47.2%; Score 76; DB 4; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.9e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVHRIETILF 32
DB 1 ISISEIKGVIVHRIEGLF 19

RESULT 7

US-09-100-414B-80
; Sequence 80, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-80

Query Match 47.2%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 2.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 14 ISITEIKGVYHRIETILF 32
Db 1 ISISEIKGVYHRIEGLIF 19

RESULT 8
US-09-303-323-80

Sequence 80, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303.323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100.414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-80

Query Match 47.2%; Score 76; DB 3; Length 35;
Best Local Similarity 84.2%; Pred. No. 2.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 14 ISITEIKGVYHRIETILF 32
Db 1 ISISEIKGVYHRIEGLIF 19

RESULT 9

US-09-770-014-80
Sequence 80, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770.014
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100.414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-80

Query Match 47.2%; Score 76; DB 4; Length 35;
Best Local Similarity 84.2%; Pred. No. 2.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 14 ISITEIKGVYHRIETILF 32
Db 1 ISISEIKGVYHRIEGLIF 19

RESULT 10

US-09-100-414B-96
Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100.414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-96

Query Match 47.2%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 3.1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVRIETILP 32
DB 1 ISISIKGVIVRIKIGILP 19

RESULT 11
US-09-303-323-96

Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-96

Query Match 47.2%; Score 76; DB 3; Length 46;
Best Local Similarity 84.2%; Pred. No. 3.1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVRIETILP 32
DB 1 ISISIKGVIVRIKIGILP 19

RESULT 12

US-09-770-014-96

Sequence 96, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-96

Query Match 47.2%; Score 76; DB 4; Length 46;
Best Local Similarity 84.2%; Pred. No. 3.1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 ISITIKGVIVRIETILP 32
DB 1 ISISIKGVIVRIKIGILP 19

RESULT 13
US-09-100-414B-60

Sequence 60, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-100-414B-60

Query Match 47.2%; Score 76; DB 3; Length 47;
Best Local Similarity 84.2%; Pred. No. 3.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 14 ISITIKGVIVHRIETILF 32
||:|||||:||||
Db 17 ISISEIKGVIVHRIEGLIF 35

RESULT 14
US-09-303-323-60
Sequence 60, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-303-323-60

Query Match 47.2%; Score 76; DB 3; Length 47;
Best Local Similarity 84.2%; Pred. No. 3.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 14 ISITIKGVIVHRIETILF 32
||:|||||:||||
Db 17 ISISEIKGVIVHRIEGLIF 35

RESULT 15
US-09-770-014-60
Sequence 60, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-770-014-60

Query Match 47.2%; Score 76; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 3.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 14 ISITIKGVIVHRIETILF 32
||:|||||:||||
Db 17 ISISEIKGVIVHRIEGLIF 35

Search completed: June 18, 2004, 20:04:45
Job time: 12.5644 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 36.1227 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294a-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITRKGYIVHRIITLIF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptoddata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	32	10	US-09-865-294-72 Sequence 72, Appl
2	150	93.2	34	14	US-09-865-294-73 Sequence 73, Appl
3	143	88.8	48	10	US-09-865-294-74 Sequence 74, Appl
4	141	87.6	30	10	US-09-865-294-71 Sequence 71, Appl
5	136	84.5	34	10	US-09-865-294-75 Sequence 75, Appl
6	129	80.1	34	10	US-09-865-294-76 Sequence 76, Appl
7	90	55.9	19	10	US-09-865-294-51 Sequence 51, Appl
8	90	55.9	31	14	US-10-076-674-6 Sequence 6, Appl
9	90	55.9	31	15	US-10-355-161A-6 Sequence 6, Appl
10	90	55.9	45	14	US-10-076-674-11 Sequence 11, Appl
11	90	55.9	45	15	US-10-355-161A-11 Sequence 11, Appl
12	90	55.9	50	14	US-10-076-674-4 Sequence 4, Appl
13	87	54.0	50	15	US-10-355-161A-4 Sequence 4, Appl
14	87	54.0	65	15	US-10-355-161A-13 Sequence 13, Appl
15	83	51.6	65	15	US-10-355-161A-12 Sequence 12, Appl

16	76	47.2	19	10	US-09-747-802-49 Sequence 49, Appl
17	76	47.2	19	10	US-09-747-802-55 Sequence 55, Appl
18	76	47.2	19	10	US-09-865-294-38 Sequence 38, Appl
19	76	47.2	19	10	US-09-865-294-41 Sequence 41, Appl
20	76	47.2	19	10	US-09-865-294-47 Sequence 47, Appl
21	76	47.2	30	10	US-09-747-802-80 Sequence 80, Appl
22	76	47.2	32	10	US-09-747-802-82 Sequence 82, Appl
23	76	47.2	34	10	US-09-747-802-78 Sequence 78, Appl
24	76	47.2	39	10	US-09-747-802-84 Sequence 84, Appl
25	76	47.2	46	10	US-09-747-802-74 Sequence 74, Appl
26	76	47.2	46	10	US-09-747-802-76 Sequence 76, Appl
27	72.5	45.0	35	9	US-09-972-475-15 Sequence 15, Appl
28	72.5	45.0	35	15	US-10-463-729-15 Sequence 15, Appl
29	71	44.1	19	10	US-09-747-802-48 Sequence 48, Appl
30	71	44.1	19	10	US-09-865-294-40 Sequence 40, Appl
31	69	42.9	19	10	US-09-747-802-46 Sequence 46, Appl
32	69	42.9	19	10	US-09-747-802-50 Sequence 50, Appl
33	69	42.9	19	10	US-09-747-802-51 Sequence 51, Appl
34	69	42.9	19	10	US-09-747-802-54 Sequence 54, Appl
35	69	42.9	19	10	US-09-747-802-56 Sequence 56, Appl
36	69	42.9	19	10	US-09-865-294-42 Sequence 42, Appl
37	69	42.9	19	10	US-09-865-294-43 Sequence 43, Appl
38	69	42.9	19	10	US-09-865-294-46 Sequence 46, Appl
39	69	42.9	19	10	US-09-865-294-48 Sequence 48, Appl
40	69	42.9	30	10	US-09-747-802-81 Sequence 81, Appl
41	69	42.9	32	10	US-09-747-802-83 Sequence 83, Appl
42	69	42.9	34	10	US-09-747-802-79 Sequence 79, Appl
43	69	42.9	39	10	US-09-747-802-85 Sequence 85, Appl
44	69	42.9	46	10	US-09-747-802-75 Sequence 75, Appl
45	69	42.9	46	10	US-09-747-802-77 Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US2003006825A1
GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 32
; TYPR: PRT
; ORGANISM: Measles virus
US-09-865-294-72
Query Match 100.0%; Score 161; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVKISITRKGYIVHRIITLIF 32
Db 1 DAEFRHDSGYEVKISITRKGYIVHRIITLIF 32
RESULT 2
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US2003006825A1
GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 34
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-73

Query Match 93.2%; Score 150; DB 10; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.1e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 32
Db 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 34

RESULT 3

US-09-865-294-74
Sequence 74, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
LENGTH: 48
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-74

Query Match 88.8%; Score 143; DB 10; Length 48;
Best Local Similarity 66.7%; Pred. No. 1.9e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

Qy 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 32
Db 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 48

RESULT 4

US-09-865-294-71
Sequence 71, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 71
LENGTH: 30
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-71

Query Match 87.6%; Score 141; DB 10; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 32
Db 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 30

RESULT 5
US-09-865-294-75
Sequence 75, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 75
LENGTH: 34
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-75

Query Match 84.5%; Score 136; DB 10; Length 34;
Best Local Similarity 85.3%; Pred. No. 1.5e-13;
Matches 29; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 32
Db 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 34

RESULT 6

US-09-865-294-76
Sequence 76, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 34
TYPE: PRT
ORGANISM: Measles virus
US-09-865-294-76

Query Match 80.1%; Score 129; DB 10; Length 34;
Best Local Similarity 85.3%; Pred. No. 1.7e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 32
Db 1 DAEFRHDSGYEVHKKISTEIKGIVVHRIETILF 34

RESULT 7

US-09-865-294-51
Sequence 51, Application US/09865294
Publication No. US20030068325A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: US/09/865,294
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 19
TYPE: PRT

ORGANISM: Measles virus
US-09-865-294-51

Query Match 55.9%; Score 90; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ISITBKGVVHRIETILF 32
DB 1 ISITBKGVVHRIETILF 19

RESULT 8
US-10-076-674-6
Sequence 6, Application US/10076674
Publication No. US20030165478A1

GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human

FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

Query Match 55.9%; Score 90; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ISITBKGVVHRIETILF 32
DB 1 ISITBKGVVHRIETILF 19

RESULT 9
US-10-355-161A-6
Sequence 6, Application US/10355161A
Publication No. US20040009897A1

GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 31
TYPE: PRT
ORGANISM: Human

FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

Query Match 55.9%; Score 90; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ISITBKGVVHRIETILF 32
DB 1 ISITBKGVVHRIETILF 19

DB 1 ISITBKGVVHRIETILF 19

RESULT 10
US-10-076-674-11
Sequence 11, Application US/10076674
Publication No. US20030165478A1

GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

Query Match 55.9%; Score 90; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ISITBKGVVHRIETILF 32
DB 1 ISITBKGVVHRIETILF 19

RESULT 11
US-10-355-161A-11
Sequence 11, Application US/10355161A
Publication No. US20040009897A1

GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 45
TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

Query Match 55.9%; Score 90; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ISITBKGVVHRIETILF 32
DB 1 ISITBKGVVHRIETILF 19

RESULT 12
US-10-076-674-4
Sequence 4, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.

```

; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

```

```

Query Match          55.9%; Score 90; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      14 ISITKGVIVHRIETILF 32
Db      1 ISITKGVIVHRIETILF 19

```

```

RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

```

```

Query Match          55.9%; Score 90; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      14 ISITKGVIVHRIETILF 32
Db      1 ISITKGVIVHRIETILF 19

```

```

RESULT 14
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13

```

```

; LENGTH: 65
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

```

```

Query Match          54.0%; Score 87; DB 15; Length 65;
Best Local Similarity 94.7%; Pred. No. 1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      14 ISITKGVIVHRIETILF 32
Db      1 ISITKGVIVHRIETILF 19

```

```

RESULT 15
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

```

```

Query Match          51.6%; Score 83; DB 15; Length 65;
Best Local Similarity 89.5%; Pred. No. 4.2e-05;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      14 ISITKGVIVHRIETILF 32
Db      1 ISITKGVIVHRIETILF 19

```

```

Search completed: June 18, 2004, 20:23:47
Job time : 37.1227 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 9.61963 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-72

Perfect score: 161

Sequence: 1 DAEFRHDSGYEVKISTIKGVIVHRIETILP 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	41.0	42	2	PN0512
2	66	41.0	57	2	B60045
3	66	41.0	57	2	B60045
4	66	41.0	57	2	B60045
5	66	41.0	57	2	B60045
6	66	41.0	57	2	B60045
7	66	41.0	57	2	B60045
8	66	41.0	82	2	B60045
9	66	41.0	695	1	Q04795
10	66	41.0	770	1	ORHUA4
11	64.5	40.1	552	2	S47034
12	64	39.8	546	1	VGNZRL
13	61	37.9	546	2	S47300
14	60	37.3	546	1	VGNZRL
15	60	37.3	546	1	VGNZRL
16	60	37.3	546	1	VGNZRL
17	59	36.6	542	2	J02223
18	59	36.6	662	1	VGNZCD
19	59	36.6	662	2	S21382
20	58.5	36.3	631	1	VGNZPD
21	58.5	36.3	631	1	A48346
22	58	36.0	282	2	P00376
23	58	36.0	282	2	P00388
24	58	36.0	534	1	JU0274
25	58	36.0	550	1	B48556
26	58	36.0	553	1	VGNZMV
27	57	35.4	33	2	S23094
28	57	35.4	220	2	T00801
29	57	35.4	229	2	P86180

30	57	35.4	695	2	A27485	Alzheimer's disease
31	57	35.4	695	2	S00550	Alzheimer's disease
32	55.5	34.5	219	2	D89923	endocannalase-like
33	55.5	34.5	356	2	D96357	hypothetical prote
34	53	32.9	175	2	D86180	hypothetical prote
35	53	32.9	221	2	F84741	probable synaptob
36	53	32.9	240	2	T47589	synaptobrevin-like
37	52	32.3	1487	2	S15904	alpha-1-proteinase
38	51.5	32.0	279	2	A11513	hypothetical prote
39	51	31.7	469	1	N1ZJMN	nicotinnase (EC 1.
40	51	31.7	747	2	JH0773	Alzheimer's disea
41	51	31.7	1451	2	B41185	alpha-2 macroglobu
42	51	31.7	1476	2	A41185	alpha-2 macroglobu
43	51	31.7	1477	2	A29952	alpha-1-proteinase
44	50	31.1	421	2	T33811	hypothetical prote
45	50	31.1	605	2	G70409	high affinity sulf

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C/Accession: PN0512

R/Shimomigashii, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, I

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm

A/Reference number: PN0512; MUID:93290653; PMID:7685598

A/Accession: PN0512

A/Molecule type: protein

A/Residues: 1-42 <SH1>

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase ;

C/Keywords: alternative splicing; amyloid

Query Match 41.0%; Score 66; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.0086;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEV 12

Db 1 DAEFRHDSGYEV 12

RESULT 2

B60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: B60045

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog.

A/Reference number: A60045; MUID:92017079; PMID:1656157

A/Accession: B60045

A/Molecule type: mRNA

A/Residues: 1-57 <JOH>

C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase ;

C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEV 12

Db 6 DAEFRHDSGYEV 17

RESULT 3

Pe0045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C/Accession: F60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: F60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: G60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: G60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56126
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: D60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: D60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56124
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12

Db 6 DAEFRHDSGYEV 17

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: A60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: A60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56125
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C/Species: Ursus maritimus (polar bear)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C/Accession: B60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: B60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 8
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C/Accession: P00438; C60045
R/Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.B.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A/Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A/Reference number: P00438; MUID:93075180; PMID:1445331
A/Accession: P00438
A/Molecule type: DNA
A/Residues: 1-82 <DAV>
A/Cross-references: GB:M83558; GB:M83657
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JON>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 41.0%; Score 66; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEV 12
 |||||
 17 DAEFRHDSGYEV 28

RESULT 9
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
 A:Reference number: A49795; MUID:91273117; PMID:1905108
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 41.0%; Score 66; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEV 12
 |||||
 597 DAEFRHDSGYEV 608

RESULT 10
 ORH004
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Containing: amyloid beta protein long; plaque form; amyloid beta protein short; vascular
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A33277; A33460; A35486; I39452; I39453; I59562; A44
 4668; A28883; A29302; A60805; J10038; S06121; A60311; A38384; S29076; S38252; S3
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The prek4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288; 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Jennaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA1830.1; PID:9871360
 A:Note: alternative splice form APP(695)
 R:Jennaire, H.G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-prot
 A:Reference number: A32277; MUID:89165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAP>
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAIC3654.1; PID:9516074
 R:Johnson, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similar
 A:Reference number: A33260; MUID:89392030; PMID:2675837
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JON>
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AA51768.1; PID:9178865
 R:Pirelli, F.; Levy, B.; Van Dunen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRB1>
 A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R:Yoshikai, S.I.; Saseki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AA59502.1; PID:9178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLMPVTPAPFPAKNGR', <YOS2>
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AA59501.1; PID:9178615
 R:Yoshikai, S.I.; Saseki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr
 A:Reference number: I39453; MUID:90260663; PMID:2111584
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AA51727.1; PID:9178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
 A:Reference number: I59562; MUID:92022553; PMID:1925564
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'P', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AA819991.1; PID:9236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wiseman, R.M.; Alonso, M.E.; Palst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Hesston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93033397; PMID:1415265
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:9257377; PIDN:AA823645.1; PID:9257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:115374)
 A:Accession: B44017
 A:Molecule type: DNA

cell fusion glycoprotein precursor - rinderpest virus (strain L)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: rinderpest virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: A28921
R:Tanikawa, K.; Yoshikawa, Y.; Yamouchi, K.
Virology 164, 523-530, 1988
A:Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A:Reference number: A28921; MUID:88219541; PMID:3285575
A:Accession: A28921
A:Molecule type: mRNA
A:Residues: 1-546 <TSU>
A:Cross-references: GB:M20870; MID:g333898; PIDN:AAA47399.1; PID:g333899
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F:105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F:109-133/Domain: transmembrane #status predicted <TN1>
F:485-513/Domain: transmembrane #status predicted <TN2>
F:25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.28;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 15 SITEIKGVIVHRIETILF 32
DB 283 SLSEIKGVIVHRLGVSVY 300

RESULT 13
S47300
gene F protein - rinderpest virus
C:Species: rinderpest virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C:Accession: S47300; PQ0865
R:Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
J. Gen. Virol. 74, 2775-2780, 1993
A:Title: Evidence for different lineages of rinderpest virus reflecting their geographic
A:Reference number: PQ0865; MUID:94103786; PMID:8277286
A:Accession: S47300
A:Molecule type: DNA
A:Residues: 1-546 <EVA>
A:Cross-references: EMBL:Z31656; MID:g535406; PIDN:CAA83482.1; PID:g535407
R:Chamberlain, R.W.; Mamway, H.M.; Hockley, E.; Shalta, M.S.; Goatley, L.; Knowles, N.J.
J. Gen. Virol. 74, 2775-2780, 1993
A:Title: Evidence for different lineages of rinderpest virus reflecting their geographic
A:Reference number: PQ0865; MUID:94103786; PMID:8277286
A:Accession: PQ0865
A:Molecule type: mRNA
A:Residues: 86-191 <CHA>
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein

Query Match 37.9%; Score 61; DB 2; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.77;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 15 SITEIKGVIVHRIETILF 32
DB 283 SLSEIKGVIVHRLGVSVY 300

RESULT 14
VGNZRX
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: rinderpest virus

C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C:Accession: A31051
R:Hu, D.; Yamakawa, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A:Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis
A:Reference number: A31051; MUID:88322864; PMID:3413983
A:Accession: A31051
A:Molecule type: genomic RNA
A:Residues: 1-546 <HSU>
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-108/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F:109-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F:109-134/Domain: transmembrane #status predicted <TN1>
F:491-513/Domain: transmembrane #status predicted <TN2>
F:25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.3%; Score 60; DB 1; Length 546;
Best Local Similarity 55.6%; Pred. No. 1.1;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 15 SITEIKGVIVHRIETILF 32
DB 283 SLSEIKGVIVHRLGVSVY 300

RESULT 15
S55386
cell fusion protein - peste-des-petites-ruminants virus (strain 75/1)
N:Alternate names: P protein
C:Species: peste-des-petites-ruminants virus
A:Variety: strain 75/1
C:Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
C:Accession: S55386
R:Meyer, G.; Diallo, A.
submitted to the EMBL Data Library, September 1994
A:Description: The nucleotide sequence of fusion protein gene of the Peste des petits r
to each virus.
A:Reference number: S55386
A:Accession: S55386
A:Molecule type: DNA
A:Residues: 1-546 <MEY>
A:Cross-references: EMBL:Z37017; MID:g854372; PIDN:CAA85451.1; PID:g854373
A:Experimental source: strain 75/1; cell line vero
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: membrane fusion

Query Match 37.3%; Score 60; DB 2; Length 546;
Best Local Similarity 61.1%; Pred. No. 1.1;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 15 SITEIKGVIVHRIETILF 32
DB 283 TLSEIKGVIVHKLIAISY 300

Search completed: June 18, 2004, 20:03:30
Job time : 9.61963 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 6.28221 Seconds

(Without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-72

Perfect score: 161
Sequence: 1 DAFPRDSGYEVKISITIKGVIVRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	41.0	57	1 A4_URSLMA	Q29149 ursus marit
2	66	41.0	58	1 A4_CANPA	Q28280 canis fam1
3	66	41.0	58	1 A4_RABIT	Q28748 cynctolagus
4	66	41.0	58	1 A4_SHEEP	Q28757 ovis aries
5	66	41.0	59	1 A4_BOVIN	Q28053 bos taurus
6	66	41.0	751	1 A4_SINSC	Q25241 s amyloid b
7	66	41.0	770	1 A4_CAVPO	Q20495 c amyloid b
8	66	41.0	770	1 A4_HUMAN	P5067 h amyloid b
9	66	41.0	770	1 A4_MACPA	P53601 m amyloid b
10	66	41.0	770	1 A4_PIG	P79307 s amyloid b
11	64	39.8	546	1 VGLF_RINDL	P10864 rinderpest
12	61	37.9	546	1 VGLF_RINDR	P11360 rinderpest
13	60	37.3	546	1 VGLF_RINDR	P11356 rinderpest
14	59	36.6	662	1 VGLF_CDVO	P12569 canine dist
15	58.5	36.3	631	1 VGLF_PHODV	P28866 phocine dis
16	58	36.0	534	1 VGLF_MEASV	P26032 measles vir
17	58	36.0	550	1 VGLF_MEASA	P26033 measles vir
18	58	36.0	550	1 VGLF_MEASA	P26034 measles vir
19	57	35.4	220	1 V725_ARATH	Q48850 arabidopsis
20	57	35.4	229	1 V726_ARATH	Q48851 arabidopsis
21	57	35.4	770	1 A4_MOUSE	P12023 m amyloid b
22	57	35.4	770	1 A4_RAT	P08592 r amyloid b
23	55.5	34.5	356	1 BCGE_ARATH	P12574 rinderpest
24	54	33.5	546	1 VGLF_RINDK	Q29149 ursus marit
25	53	32.9	219	1 V721_ARATH	Q48850 arabidopsis
26	53	32.9	221	1 V722_ARATH	Q48851 arabidopsis
27	53	32.9	240	1 V727_ARATH	Q48852 arabidopsis
28	51	31.7	469	1 NIFN_BRAJA	P26507 brahyrhizob
29	51	31.7	1451	1 A2M2_MOUSE	P28666 mus musculu
30	51	31.7	1476	1 A2M1_MOUSE	P28665 mus musculu
31	51	31.7	1477	1 A113_RAT	P14046 ratius norv
32	50	31.1	506	1 MATK_RHOFR	P62984 rhododendro
33	50	31.1	529	1 VGLF_MEASI	P26031 measles vir

34	49	30.4	244	1 YSCJ_YEREN	Q01251 yersinia en
35	49	30.4	244	1 YSCJ_YERPE	Q00926 yersinia pe
36	49	30.4	481	1 GATB_FUSNN	Q01600 fusobacteri
37	49	30.4	506	1 MATK_RHOTS	Q62991 rhododendro
38	48	29.8	254	1 PMG3_HUMAN	Q80097 homo sapien
39	48	29.8	254	1 PMG3_PANTR	Q80098 pan troglod
40	48	29.8	316	1 YMK1_CABEL	P74509 caenorhadi
41	48	29.8	364	1 Y955_SYNY3	P74328 synechocyst
42	47.5	29.5	367	1 BCAT7_ARATH	Q91pm8 arabidopsis
43	47	29.2	711	1 LKX3_HUMAN	Q9byj1 homo sapien
44	46.5	28.9	181	1 YB33_ARCFU	Q28839 archaeoglob
45	46.5	28.9	196	1 GCH2_YERPE	Q82et0 yersinia pe

ALIGNMENTS

RESULT 1	ID	A4_URSLMA	STANDARD;	PRT;	57 AA.
AC	Q29149;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid				
DE	protein (Beta-A4P) (A-beta)] (Fragment).				
GN	APP.				
OS	Ursus maritimus (Polar bear) (Tralacros maritimus).				
OC	Bakartota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Butheria; Carnivora; Fissipedia; Ursidae; Ursus.				
OX	NCBI_TaxID=29073;				
FM	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=92017079; PubMed=1656157;				
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;				
RT	"Conservation of the sequence of the Alzheimer's disease amyloid				
RT	peptide in dog, polar bear and five other mammals by cross-species				
RT	polymerase chain reaction analysis."				
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).				
CC	-1- FUNCTION: Functional neuronal receptor which couples to				
CC	intracellular signaling pathway through the GTP-binding protein				
CC	G(O) (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: Belongs to the APP family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL; X56128; CA93593.1; -				
DR	PIR; B60045; B60045.				
DR	HSSP; P05067; IBA4.				
DR	InterPro; IPR008155; A4_APP.				
DR	InterPro; IPR001255; Beta-APP.				
DR	Pfam; PF03494; Beta-APP; 1.				
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.				
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.				
KM	GLYCOPROTEIN; Amyloid; Neurone; Transmembrane.				
FT	NON TER	1			
FT	CHAIN	1			
FT	DOMAIN	6	48		BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	<1	33		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	34	57		POTENTIAL.
FT	NON TER	57			
SQ	SEQUENCE	57 AA; 6172 MW; 8420988BA82DFA CRC64;			
Query Match	41.0%;	Score 66;	DB 1;	Length 57;	
Best local similarity	100.0%;	Pred. No. 0.0046;			
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

Oy 1 DAEFRHDSGYEV 12
 |||||
 Db 6 DAEFRHDSGYEV 17

RESULT 2
 A4_CANFA STANDARD; PRT; 58 AA.

AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-Ap) (A-beta)] (fragment).
 GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity). Type I membrane protein.
 CC -1- SUBCELLULAR LOCATION: Belongs to the APP family.
 CC -1- SIMILARITY: Belongs to the APP family.

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 or send an email to license@isb-sib.ch).

CC EMBL; X56125; CAJ39590.1; -
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49
 FT DOMAIN <1 34 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT TRANSMEM 35 58 EXTRACELLULAR (POTENTIAL).
 FT NON_TER 58 58 POTENTIAL.
 SO SEQUENCE 58 AA; 6285 MW; 8469D488A2B12D7A CRC64;

Query Match 41.0%; Score 66; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEV 12
 |||||
 Db 7 DAEFRHDSGYEV 18

RESULT 3
 A4_RABIT STANDARD; PRT; 58 AA.

AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-APP) (A-beta)] (fragment).
 GN APP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity). Type I membrane protein.
 CC -1- SUBCELLULAR LOCATION: Belongs to the APP family.
 CC -1- SIMILARITY: Belongs to the APP family.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; X56129; CAJ39594.1; -
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48
 FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SO SEQUENCE 58 AA; 6300 MW; F434209D88BA82D CRC64;

Query Match 41.0%; Score 66; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEV 12
 |||||
 Db 6 DAEFRHDSGYEV 17

RESULT 4
 A4_SHEEP STANDARD; PRT; 58 AA.

AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-APP) (A-beta)] (fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.

CC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.

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or send an email to license@ebi.ac.uk).

CC
CC EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON TER 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT PT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88BA02D CRC64;

Query Match 41.0%; Score 66; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
Db 6 DAEFRHDSGYEV 17

RESULT 5
A4_BOVIN STANDARD; PRT; 59 AA.
ID_A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
OS Bos taurus (Bovine).
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157.
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SIMILARITY: Belongs to the APP family).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.

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CC or send an email to license@ibt-sib.ch).

CC
DR EMBL; X56124; CAJ39589.1; -.
DR EMBL; X56126; CAJ39591.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neuron; Transmembrane.
KW NON_TER
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 7 19 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; P43469D489A2B12D CRC64;

Query Match 41.0%; Score 66; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
Db 7 DAEFRHDSGYEV 18
|||||
|

RESULT 6
A4_SAIISC STANDARD; PRT; 751 AA.
ID_A4_SAIISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE Beta-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
OS Saimiri sciureus (common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy B., Amotim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tif60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and JIP (By
CC similarity). Inhibits G10 alpha kinase activity (By similarity).

Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APPA family, MAPKIP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FRL1, APPB1, IBI, KMS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAP1 via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:

Event-Alternative splicing: Named isoforms=2;

Comment-Additional isoforms seem to exist;

Name=APP770;

Isoid=Q95241-1; Sequence=Displayed;

Name=APP695;

Isoid=Q95241-2; Sequence=Not described;

-1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-1- DOMAIN: The NPYX sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPYX motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPYX site is also involved in clathrin-mediated endocytosis (By similarity).

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/cathepsin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-1- PTM: N- and O-glycosylated (By similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: S81024; AAD14347.1; -

HSSP: P05067; IAMP.

InterPro: IPR008155; A4_APP.

InterPro: IPR008154; A4_extra.

InterPro: IPR001255; Beta-APP.

InterPro: IPR002223; Kunitz_BPTI.

Pfam: PF02177; A4_EXTRA; 1.

Pfam: PF03494; Beta-APP; 1.

Pfam: PF00014; Kunitz_BPTI; 1.

PRINTS: PR00203; AMYLOIDA4.

PRINTS: PR00759; BASICPTASE.

ProDom: PD000222; Kunitz_BPTI; 1.

SMART: SM00006; A4_EXTRA; 1.

SMART: SM00131; KO; 1.

PROSITE: PS00319; A4_EXTRA; 1.

PROSITE: PS00320; A4_INTRA; 1.

PROSITE: PS00280; BPTI_KUNITZ_1; 1.

PROSITE: PS50279; BPTI_KUNITZ_2; 1.

Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation; Proteoglycan; Amyloid; Alternative splicing.

KW SIGNAL; 1

FT CHAIN 1 751

FT CHAIN 18 668

FT CHAIN 18 652

FT CHAIN 653 751

FT CHAIN 653 694

FT CHAIN 653 692

FT CHAIN 659 751

FT CHAIN 659 694

FT CHAIN 669 692

FT CHAIN 693 751

FT CHAIN 695 751

FT CHAIN 702 751

FT CHAIN 721 751

FT CHAIN 18 680

FT TRANSMEM 681 704

FT DOMAIN 705 751

FT DOMAIN 96 110

FT DOMAIN 181 188

FT DOMAIN 291 341

FT DOMAIN 316 344

FT DOMAIN 363 428

FT DOMAIN 504 521

FT DOMAIN 713 732

FT DOMAIN 230 260

FT DOMAIN 274 280

FT SITE 144 144

FT ACT_SITE 301 302

FT SITE 652 653

A4 PROTEIN.

SOLUBLE APP-ALPHA (POTENTIAL).

SOLUBLE APP-BETA (POTENTIAL).

C99 (POTENTIAL).

BETA-AMYLOID PROTEIN 42 (POTENTIAL).

BETA-AMYLOID PROTEIN 40 (POTENTIAL).

C83 (POTENTIAL).

B1(42) (POTENTIAL).

B3(40) (POTENTIAL).

GAMMA-CTF(59) (POTENTIAL).

GAMMA-CTF(57) (POTENTIAL).

GAMMA-CTF(50) (POTENTIAL).

C31 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CTOPLASMIC (POTENTIAL).

HEPARIN-BINDING (BY SIMILARITY).

ZINC-BINDING (BY SIMILARITY).

BPTI/KUNITZ INHIBITOR.

HEPARIN-BINDING (BY SIMILARITY).

HEPARIN-BINDING (BY SIMILARITY).

COLLAGEN-BINDING (BY SIMILARITY).

INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).

ASP/GLU-RICH (ACIDIC).

POLY-THR.

REQUIRED FOR COPPER (II) REDUCTION (BY SIMILARITY).

REACTIVE BOND.

CLEAVAGE (BY BETA-SECRETASE)

PT	SITE	653	654	(BY SIMILARITY).
FT	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).			
TT	CLEAVAGE (BY ALPHA-SECRETASE)			
FT	CLEAVAGE (BY SIMILARITY).			
FT	INVOLVED IN FREE RADICAL PROPAGATION			
FT	(BY SIMILARITY).			
FT	INVOLVED IN OXIDATIVE REACTIONS			
FT	(BY SIMILARITY).			
FT	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)			
FT	(BY SIMILARITY).			
FT	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)			
FT	(BY SIMILARITY).			
FT	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)			
FT	(BY SIMILARITY).			
FT	BASOLATERAL SORTING SIGNAL			
FT	(BY SIMILARITY).			
FT	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)			
FT	(BY SIMILARITY).			
FT	ENDOCYTOSIS SIGNAL.			
FT	NPKY MOTIF.			
FT	SITE	738	741	
FT	SITE	740	743	
Qy	Query Match	41.0%;	Score 66;	DB 1; length 751;
Dd	Best Local Similarity	100.0%;	Pred. No. 0.071;	
Oy	Matches	12;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
	1 DAEPFHDSGYEV	12		
	DAEPRHDSGYEV	664		
RESULT 7	A4_CAVPO	STANDARD;	PRT;	770 AA.
ID	A4_CAVPO	060495;		
AC	Q60495;	Q60496;		
DT	10-OCT-2003	(Rel. 42,	Created)	
DT	10-OCT-2003	(Rel. 42,	Last sequence update)	
DT	10-OCT-2003	(Rel. 42,	Last annotation update)	
DE	Amyloid beta A4 protein precursor (APP) (ABPP) {Alzheimer's disease			
DE	Amyloid protein homolog} [Contains: Soluble APP-alpha (S-APP-alpha);			
DE	Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid			
DE	protein 42 (Beta-AAP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);			
DE	P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-			
DE	CTF(57) (Gamma-secretase C-terminal fragment 57); C31).			
GN	APP.			
OS	Cavia porcellus (Guinea pig) .			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.			
NCBI_TaxId=10141;				
RN	[1]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RC	TISSUE=Brain, and Liver;			
RX	MEDLINE=97236426; PubMed=9116031;			
RA	Beck W., Mueller D., Bigl V.;			
RL	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and			
RL	alternative splicing."			
RL	Biochim. Biophys. Acta 1351:17-21(1997).			
RN	[2]			
RP	INTERACTION OF BETA-APP40 WITH APOB.			
RX	MEDLINE=98007700; PubMed=9349544;			
RA	Martel C.L., Macic J.B., Matsubara E., Governale S., Miguel C.,			
RA	Miao W., McComb J.G., Frangione B., Giulio J., Zlokovic B.V.;			
RT	"Isoform-specific effects of apolipoproteins E2, E3, and E4 on			
RT	cerebral capillary sequestration and blood-brain barrier transport of			
RL	circulating Alzheimer's amyloid beta."			
RL	J. Neurochem. 69:1995-2004(1997).			
RN	[3]			
RP	PROCESSING.			
RX	MEDLINE=20084499; PubMed=10619481;			
RA	Beck M., Bruecker M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,			
RA	Bigl V.;			
RT	"Guinea-pig primary cell cultures provide a model to study expression			
RT	and amyloidogenic processing of endogenous amyloid precursor			
RT	protein."			

RL Neuroscience 95:243-254(2000) .
 [4]
 RN GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007;
 RA Plimix I., Musunuru V., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.,
 RT *A novel gamma -secretase assay based on detection of the putative
 C-terminal fragment-gamma of amyloid beta protein precursor. ",
 RL J. Biol. Chem. 276:481-487(2001) .
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Trip6 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity) .
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity) .
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Apficans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity) .
 CC -1- FUNCTION: The gamma-CTF peptides as "well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity) .
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MARK3BP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, PRLR, APPBP1, IBI, KNS2
 CC (via its TPR domain), APPBP2 (via BASS) and DDB1 (By similarity)
 CC Associates with microtubules in the presence of APP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC APOB3 appears to be the preferred amyloid binding isoform, while
 CC the apoB4 isoform-beta-ApA40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity) .
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bvent-Alternative splicing; Named isoforms=2;
 CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC apficans:
 CC Name=APP70;
 CC ISOId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC ISOId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are

predominantly expressed in peripheral organs such as muscle and liver.

-1- INDUCTION: Increased levels during neuronal differentiation.

-1- DOMAIN: The basolateral sorting signal (Bass) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue (By similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTFbeta).

-1- PTM: Proteolytically cleaved by caspase-3 during neuronal apoptosis (By similarity).

-1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to the L-APP isoforms produces the APP proteoglycan core proteins, the apolipans (By similarity).

-1- PTM: Phosphorylation on tyrosine, threonine and serine residues is neuron-specific (By similarity). Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins.

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates.

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; X97631; CAA66230.1; -
EMBL; X99198; CAA67589.1; -
HSSP; P05067; 1BA4
InterPro; IPR008155; A4_APP
InterPro; IPR008154; A4_extra
InterPro; IPR002223; Kunitz_BPTI
Pfam; PF00014; Kunitz_BPTI; 1
PRINTS; PR00203; AMYLOIDA4
PRINTS; PR00759; BASICTPASE
ProDom; PD000222; Kunitz_BPTI; 1
SMART; SM00006; A4_EXTRA; 1
SMART; SM00131; KU; 1
PROSITE; PS00319; A4_EXTRA; 1
PROSITE; PS00320; A4_INTRA; 1
PROSITE; PS00280; BPTI_KUNITZ_1; 1
PROSITE; PS00729; BPTI_KUNITZ_2; 1
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;

KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
FT CHAIN 688 713 P3(42) (BY SIMILARITY).
FT CHAIN 688 711 P3(40) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(57) (BY SIMILARITY).
FT CHAIN 714 770

Query Match
Best local similarity 100.0%; Pred. No. 0.073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPRHDSGYEV 12
Db 672 DAEPRHDSGYEV 683

RESULT 8
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BRT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UCS6;
DT 13-AUG-1987 (Rel. 05; Created)
DT 01-NOV-1991 (Rel. 20; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Precursor
DE nexin-II) (PN-II) (APP1) (PreA4) (Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaitre H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor".
RT Nature 325:733-736(1987).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhite P., Schilling J., Miller J., Han D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors".
RT Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons".
RT Nucleic Acids Res. 17:517-522(1989).

[14] RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 gene.";
 RL Gene 87:257-263 (1990).
 RN
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292 (1991).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809 (1992).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tanahara F., Funahata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808 (1997).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108 (2003).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancereas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg R., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heleh P.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Raha S.S., Logucliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
 RA Villalona D.K., Wozny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schenker A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351 (1988).
 RN
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RX Nucleic Acids Res. 16:11402-11402 (1988).

[12] RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304 (1989).
 RN
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.B., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514 (1987).
 RN
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653 (1989).
 RN
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194 (1987).
 RN
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.B., McClatchey A.J., Lamperti E.D., Villa-Komaroff L.,
 RA Guealla J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530 (1988).
 RN
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532 (1988).
 RN
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.B.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933 (1988).
 RN
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behler D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620 (1996).
 RN
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHR-717; AD ILE-717
 AND AD GLY-717.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Demian R.B., Rosenczwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103 (1993).
 RN
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;

RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.; Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [22]

Query March 41.0%; Score 66; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.073; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
 Db 672 DAEFRHDSGYEV 683

RESULT 9
 A4_MACPFA STANDARD; PRT; 770 AA.
 ID A4_MACPFA
 AC P53601: 095K07;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid beta A4 protein precursor) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(55)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 RN NCB1_TaxID=9541;
 RX [1]
 RP SEQUENCE FROM N.A. (ISOPFORMS APP695 AND APP770).
 RC TISSUE=Cerebellum; PubMed=1905108;
 RX MEDLINE=91273117;
 RA "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease";
 RL Am. J. Pathol. 138:1423-1435(1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptotic-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPT domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding

CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, APPB1, APPB1, IBI, KNS2
 CC (via its TPR domain) (By similarity). APPB2 (via BASS) and DBB1.
 CC In vitro, it binds MAPT via the MT-binding domain (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC Name=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC EMBL; MS8727; AAA36829.1; -
 DR EMBL; MS8726; AAA36828.1; -
 DR HSPF; P05067; IAAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTAS.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 DR Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KM Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KM Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KM Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT CHAIN 18 667
 FT CHAIN 18 671
 FT CHAIN 672 770
 FT CHAIN 672 713
 FT CHAIN 672 711
 FT CHAIN 668 770
 FT CHAIN 668 713
 FT CHAIN 668 711
 FT CHAIN 712 770
 FT CHAIN 714 770
 FT CHAIN 721 770
 FT CHAIN 740 770
 FT CHAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 231 341
 FT DOMAIN 331 423
 FT DOMAIN 431 522
 FT DOMAIN 523 540
 FT DOMAIN 732 751
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT ACT SITE 301 302
 FT SITE 611 672
 FT SITE 672 673
 FT SITE 667 668
 FT SITE 704 704
 FT SITE 706 706
 FT SITE 711 712
 FT SITE 713 714
 FT SITE 720 721
 FT SITE 724 734
 FT SITE 739 740

AMYLOID BETA A4 PROTEIN.
 SOLUBLE APP-ALPHA (POTENTIAL).
 SOLUBLE APP-BETA (POTENTIAL).
 C99 (POTENTIAL).
 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 C83 (POTENTIAL).
 P3(42) (POTENTIAL).
 P3(40) (POTENTIAL).
 GAMMA-CTF(59) (POTENTIAL).
 GAMMA-CTF(57) (POTENTIAL).
 GAMMA-CTF(50) (POTENTIAL).
 C31 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOSOLIC (POTENTIAL).
 HEPARIN-BINDING (BY SIMILARITY).
 ZINC-BINDING (BY SIMILARITY).
 BPTI/KUNITZ INHIBITOR.
 HEPARIN-BINDING (BY SIMILARITY).
 HEPARIN-BINDING (BY SIMILARITY).
 HEPARIN-BINDING (BY SIMILARITY).
 COLLAGEN-BINDING (BY SIMILARITY).
 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 ASP/GHU-RICH (ACIDIC).
 POLY-THR.
 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 REACTIVE BOND (BY SIMILARITY).
 CLEAVAGE (BY BETA-SECRETASE)
 (BY SIMILARITY).
 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 CLEAVAGE (BY ALPHA-SECRETASE)
 (BY SIMILARITY).
 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 (BY SIMILARITY).
 BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 41.0%; Score 66; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.073;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 Db 672 DAEFRHDSGYEV 683

RESULT 10
 ID A4_PIG STANDARD; PRT; 770 AA.
 AC P75307; Q29023; Q9TU10;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RA TISSUE=Small intestine;
 RA Winteroe A.R., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine CDNA
 RT library." (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RA TISSUE=Brain;
 RX MEDLINE=92017079; Pubmed=1656157;
 RA Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinase I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or its potentialized through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

cytoplasmic proteins, including APPB family members, the APPA family, MAPKIP1, and SHC1. Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FRLL1, APPB1, IBI, XMS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ARP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via a clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, Presenilin/Notch-1-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-1- PTM: N- and O-glycosylated (By similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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DR EMBL; AB032550; BAA84580.1; -

DR	EMBL; Z84022; CAB06313.1; -	1	17	BY SIMILARITY.
DR	EMBL; X56127; CAA39592.1; -	1	770	AMYLOID BETA A4 PROTEIN.
DR	HSSP; P05067; IAAP.	18	687	SOLUBLE APP-ALPHA (POTENTIAL).
DR	InterPro; IPR008155; A4_APP.	18	671	SOLUBLE APP-BETA (POTENTIAL).
DR	InterPro; IPR008154; A4_extra.	672	770	C99 (BY SIMILARITY).
DR	InterPro; IPR002223; Kunitz_BPTI.	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
DR	Pfam; PF02177; A4_EXTRA; 1.	672	711	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
DR	PRINTS; PR00203; AMYLOID4.	688	770	C93 (BY SIMILARITY).
DR	PRINTS; PR00759; BASICPTASE.	688	713	P3(42) (BY SIMILARITY).
DR	ProDom; PD000222; Kunitz_BPTI.	712	770	P3(40) (BY SIMILARITY).
DR	SMART; SM00006; A4_EXTRA; 1.	714	770	GAMMA-CTF(59).
DR	SMART; SM00131; KU; 1.	721	770	GAMMA-CTF(57).
DR	PROSITE; PS00319; A4_EXTRA; 1.	740	770	GAMMA-CTF(50) (BY SIMILARITY).
DR	PROSITE; PS00320; A4_INTRA; 1.	740	770	C31 (DURING APOPTOSIS) (BY SIMILARITY).
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.	18	699	EXTRACELLULAR (POTENTIAL).
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.	700	723	POTENTIAL.
KW	Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neutrone; Heparin binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;	724	770	CYTOPLASMIC (POTENTIAL).
KW	Amyloid.	724	770	HEPARIN-BINDING (BY SIMILARITY).
FT	SIGNAL	724	770	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	135	155	COPPER-BINDING (BY SIMILARITY).
FT	CHAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	CHAIN	231	341	BPTI/KUNITZ INHIBITOR.
FT	CHAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	CHAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	DOMAIN	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT	ACT SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT	SITE	672	673	(BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	704	704	CLEAVAGE (BY ALPHA-SECRETASE)
FT	SITE	706	706	(BY SIMILARITY).
FT	SITE	711	712	IMPLICATED IN FREE RADICAL PROPAGATION
FT	SITE	713	714	(BY SIMILARITY).
FT	SITE	720	721	INVOLVED IN OXIDATIVE REACTIONS
FT	SITE			(BY SIMILARITY).
FT	SITE			CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT	SITE			(BY SIMILARITY).
FT	SITE			CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT	SITE			(BY SIMILARITY).
FT	SITE			CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT	SITE			(BY SIMILARITY).

Query Match 41.0%; Score 66; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.073;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DAEFRHDSGYEV 12
 672 DAEFRHDSGYEV 683

```

RESULT 11
VGLF_RINDL STANDARD; PRT; 546 AA.
AC P10864;
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-JUL-1989 (Rel. 11, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain L) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11243;
OK NCBI
RN SEQUENCE FROM N.A.
RP MEDLINE=88219541; PubMed=3285575;
RA Teufelmann K., Yoshikawa Y., Yamamoto K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
sequence of the F mRNA, and several features of the F protein.";
Virology 164:523-530(1988).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.
-----
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or send an email to license@isb-sib.ch).
-----
DR EMBL: M20870; AAA47399.1; -.
DR PIR: A28921; VGNZRL.
DR HSSP: P04849; ISVP.
DR InterPro: IPR000776; Fusion gly.
DR Pfam: PF00523; Fusion gly.1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SQ
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58911 MW; 985029418F28F7B5 CRC64;

Query Match 39.8%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.1;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain BRT1) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=39007;
OK NCBI
RN SEQUENCE FROM N.A.
RP MEDLINE=95088609; PubMed=796154;
RA Evans S.A., Barton M.D., Chamberlain R.W., Goatsley L., Barrett T.;
RT "Nucleotide sequence comparisons of the fusion protein gene from
ruminant and attenuated strains of rinderpest virus.";
J. Gen. Virol. 75:3611-3617(1994).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.
-----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL: Z31656; CA83482.1; -.
DR PIR: S47300; S47300.
DR HSSP: P04849; ISVP.
DR InterPro: IPR000776; Fusion gly.
DR Pfam: PF00523; Fusion gly.1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SQ
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58418 MW; 38B5398B9344F401 CRC64;

Query Match 37.9%; Score 61; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.28;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
VGLF_RINDL STANDARD; PRT; 546 AA.
AC P41360;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain RBOK) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11243;
OK NCBI
RN SEQUENCE FROM N.A.
RP MEDLINE=88219541; PubMed=3285575;
RA Teufelmann K., Yoshikawa Y., Yamamoto K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
sequence of the F mRNA, and several features of the F protein.";
Virology 164:523-530(1988).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.
-----
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
-----
DR EMBL: M20870; AAA47399.1; -.
DR PIR: A28921; VGNZRL.
DR HSSP: P04849; ISVP.
DR InterPro: IPR000776; Fusion gly.
DR Pfam: PF00523; Fusion gly.1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SQ
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58911 MW; 985029418F28F7B5 CRC64;

Query Match 39.8%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.1;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13
VGLF_RINDL STANDARD; PRT; 546 AA.
AC P41356;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain RBOK) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11243;
OK NCBI
RN SEQUENCE FROM N.A.
RP MEDLINE=88219541; PubMed=3285575;
RA Teufelmann K., Yoshikawa Y., Yamamoto K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
sequence of the F mRNA, and several features of the F protein.";
Virology 164:523-530(1988).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL: M20870; AAA47399.1; -.
DR PIR: A28921; VGNZRL.
DR HSSP: P04849; ISVP.
DR InterPro: IPR000776; Fusion gly.
DR Pfam: PF00523; Fusion gly.1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
SQ
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58418 MW; 38B5398B9344F401 CRC64;

Query Match 37.9%; Score 61; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.28;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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OX NCBI_TaxID=36409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9508609; PubMed=7996154;
 RA Evans S.A., Baron M.D., Chamberlain R.W., Coatsley L., Barrett T.;
 RT "Nucleotide sequence comparisons of the fusion protein gene from
 RT virulent and attenuated strains of rinderpest virus.";
 RL J. Gen. Virol. 75:3611-3617(1994).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z30700; CAA83186.1; -;
 CC EMBL; Z30697; CAA83181.1; -;
 CC PIR; S47305; S47305.
 CC HSSP; P04849; 1SVF.
 CC InterPro; IPR000776; Fusion_gly.
 CC Pfam; PF00523; fusion_gly; 1.
 CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 546 FUSION GLYCOPROTEIN F0.
 CC CHAIN 20 108 F2 PROTEIN.
 CC CHAIN 109 546 F1 PROTEIN.
 CC DOMAIN 104 108 ARG/LYS-RICH (BASIC).
 CC TRANSMEM 109 133 POTENTIAL.
 CC TRANSMEM 484 513 POTENTIAL.
 CC DOMAIN 514 517 ARG/LYS-RICH (BASIC).
 CC DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 CC CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 546 AA; 58705 MW; ED3DF8AFDEBC95 CRC64;
 SQ
 Query Match 37.3%; Score 60; DB 1; Length 546;
 Best Local Similarity 55.6%; Pred. No. 0.4;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 15 SITRIKGVIVHRIETLP 32
 DB 283 SLSTIKGVIVHRIEGLVSY 300
 RESULT 14
 VGLF CDVO STANDARD; PRT; 662 AA.
 AC P12569; Q65991;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Canine distemper virus (strain Onderstepoort) (CDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirinae;
 OC NCBI_TaxID=11233;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=88129050; PubMed=3433924;
 RA Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
 RT "The nucleotide sequence of the gene encoding the F protein of canine

RT distemper virus: a comparison of the deduced amino acid sequence with
 RT other paramyxoviruses.";
 RL Virus Res. 8:373-386(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93227696; PubMed=8470428;
 RA Wild T.F., Bernard A., Spennert D., Valleval D., Drillean R.;
 RT "Vaccination of mice against canine distemper virus-induced
 RT encephalitis with vaccinia virus recombinants encoding measles or
 RT canine distemper virus antigens.";
 RL Vaccine 11:438-444(1993).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC -----
 CC EMBL; M21849; AAA42878.1; -;
 CC EMBL; X65509; CAA46481.1; -;
 CC PIR; J50321; VGNZCD.
 CC PIR; S21382; S21382.
 CC HSSP; P04849; 1SVF.
 CC InterPro; IPR000776; Fusion_gly.
 CC Pfam; PF00523; fusion_gly; 1.
 CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 CC SIGNAL 1 662
 CC CHAIN 2 662 FUSION GLYCOPROTEIN F0.
 CC CHAIN 225 662 F2 PROTEIN F2.
 CC CHAIN 225 662 F1 PROTEIN F1.
 CC TRANSMEM 606 629 POTENTIAL.
 CC DISULFID 180 307 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 CC CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 3 3 R -> K (IN REF. 2).
 CC CONFLICT 140 140 D -> N (IN REF. 2).
 CC CONFLICT 152 152 N -> S (IN REF. 2).
 CC CONFLICT 171 171 I -> M (IN REF. 2).
 CC CONFLICT 174 174 A -> V (IN REF. 2).
 CC CONFLICT 662 662 L -> H (IN REF. 2).
 CC SEQUENCE 662 AA; 72970 MW; FB2C81C9797805F0 CRC64;
 SQ
 Query Match 36.6%; Score 59; DB 1; Length 662;
 Best Local Similarity 50.0%; Pred. No. 0.68;
 Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 15 SITRIKGVIVHRIETLP 32
 DB 399 TLSEVKGIVHRIEGLVSY 416
 RESULT 15
 VGLF PHODV STANDARD; PRT; 631 AA.
 AC P28866;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Plocine distemper virus (PDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

Search completed: June 18, 2004, 19:59:37
 Job time : 7.28221 secs

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OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate DK88-4A;
RX MEDLINE=92113538; PubMed=1765768;
RA Koevamees J., Blixenkron-Moeller M., Sharma B., Oerfell C.,
  Norby E.;
RT "The nucleotide sequence and deduced amino acid composition of the
  haemagglutinin and fusion proteins of the morbillivirus phocid
  distemper virus."
RT J. Gen. Virol. 72:2959-2966(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulester/88;
RX MEDLINE=92398437; PubMed=1524494;
RA Curran M.D., Lu Y.J., Rima B.K.;
RT "The fusion protein gene of phocine distemper virus: nucleotide and
  deduced amino acid sequences and a comparison of morbillivirus fusion
  proteins."
RT Arch. Virol. 126:159-169(1992).
RN [3]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=Ulester/88;
RX MEDLINE=91089508; PubMed=2264246;
RA Curran M.D., Loan D.O., Rima B.K., Kennedy S.;
RT "Nucleotide sequence analysis of phocine distemper virus reveals its
  distinctness from canine distemper virus."
RT Vet. Rec. 127:430-431(1990).
CC -I- FUNCTION: This protein directs fusion of viral and cellular
  membranes.
CC -I- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
  LINKED BY A DISULFIDE BOND.
CC -I- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
  family.
CC -----
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CC -----
DR EMBL, D10371; BAA01206.1; -.
DR PIR, A48346; A48346.
DR PIR, JQ1368; VGNZPD.
DR HSSP, P04849; ISVF.
DR InterPro, IPR000776; Fusion_gly.
DR Pfam, PF00523; fusion_gly.1.
KM Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1
FT CHAIN ? 631
FT CHAIN ? 188
FT CHAIN ? 631
FT DISULFID 149 276
FT TRANSMEM 89 106
FT TRANSMEM 194 212
FT TRANSMEM 575 595
FT TRANSMEM 110 110
FT CARBOHYD 142 142
FT CARBOHYD 148 148
FT CONFLICT 63
SQ SEQUENCE 631 AA; 68873 MW; DFC87CD942689B8 CRC64;

Query Match 36.3%; Score 58.5; DB 1; Length 631;
Best local similarity 40.0%; Pred. No. 0.77;
Matches 12; Conservative 8; Mismatches 5; Indels 5; Gaps 1;

QY 8 SGTEVKIST-----TRIKGYIVRIETILP 32
DB 356 SGKEIVLISISYPTLSKGVVHRLAVSY 385

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OW protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 31.0184 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-72

Sequence: 1 DAEFRDSDGYEVKISITIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	41.6	82	4	Q16014
2	66	41.0	19	4	Q9UC8
3	66	41.0	28	4	Q9UCD1
4	66	41.0	30	4	Q9UCA9
5	66	41.0	33	4	Q9UC33
6	66	41.0	82	4	Q16020
7	66	41.0	82	4	Q16019
8	66	41.0	113	13	Q8UH58
9	66	41.0	534	13	Q93296
10	66	41.0	569	13	Q9PVL1
11	66	41.0	695	13	Q9DGL8
12	66	41.0	751	13	Q9DCJ7
13	64.5	40.1	552	12	Q66147
14	61.5	38.2	552	12	Q66409
15	61.5	38.2	552	12	Q56852
16	61	37.9	35	4	Q8W299

17	61	37.9	546	12	Q91HA5	Q91HA5 rinderpest
18	60	37.3	546	12	Q84926	Q84926 peste-des-p
19	59	36.6	528	12	Q9YJW9	Q9YJW9 canine dist
20	59	36.6	530	12	Q8QV06	Q8QV06 canine dist
21	59	36.6	662	12	Q9DXZ2	Q9DXZ2 canine dist
22	59	36.6	662	12	Q91KN3	Q91KN3 canine dist
23	59	36.6	662	12	Q9YKX7	Q9YKX7 canine dist
24	59	36.6	662	12	Q89327	Q89327 canine dist
25	58	36.0	534	12	Q04243	Q04243 measles vir
26	58	36.0	537	12	Q04242	Q04242 measles vir
27	58	36.0	545	12	Q9PXA4	Q9PXA4 measles vir
28	58	36.0	550	12	P90J31	P90J31 measles vir
29	58	36.0	550	12	Q9QEX0	Q9QEX0 measles vir
30	58	36.0	550	12	Q9QEM9	Q9QEM9 measles vir
31	58	36.0	550	12	P90330	P90330 measles vir
32	58	36.0	550	12	Q9QEW7	Q9QEW7 measles vir
33	58	36.0	550	12	Q9QEW4	Q9QEW4 measles vir
34	58	36.0	550	12	Q9Y495	Q9Y495 measles vir
35	58	36.0	550	12	Q8V049	Q8V049 measles vir
36	58	36.0	550	12	Q9YJ94	Q9YJ94 measles vir
37	58	36.0	550	12	Q9QEX1	Q9QEX1 measles vir
38	58	36.0	550	12	Q9QEW8	Q9QEW8 measles vir
39	58	36.0	553	12	Q93055	Q93055 measles vir
40	58	36.0	553	12	Q9IC36	Q9IC36 measles vir
41	58	36.0	553	12	P88973	P88973 measles vir
42	58	36.0	553	12	Q83536	Q83536 measles vir
43	58	36.0	553	12	Q11383	Q11383 measles vir
44	58	36.0	553	12	Q9IFK2	Q9IFK2 measles vir
45	58	36.0	553	12	Q83533	Q83533 measles vir

ALIGNMENTS

RESULT 1
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RT Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor".
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NOW_TER 1
FT NOW_TER 1
SQ SBDQENCE 82 AA; 8972 MW; F534MA5B3EM9230A CRC64;

Query Match 41.6%; Score 67; DB 4; Length 82;
Best Local Similarity 41.3%; Pred. No. 0.04;
Matches 19; Conservative 5; Mismatches 8; Indels 14; Gaps 3;

QY 1 DAEFRDSDGYEVKISITIKGVIVHRIETILF 32
DB 18 DAEFRDSDGYEVHOKIVFPAEDVGSNKGATIGLWGVATVIF 63

RESULT 2
Q9UC8

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ID 09UC8      PRELIMINARY;      PRT;      19 AA.
AC 09UC8:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Beta-amyloid-(1-42) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94068497; PubMed=8248178;
RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA Gowing B., Ball M.J.;
RT "beta-amyloid-(1-42) is a major component of cerebrovascular amyloid
RT deposits: implications for the pathology of Alzheimer disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR HSP; P05067; IAMB.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 19 AA; 2315 MW; 05B02B3FEDBCE38 CRC64;

Query Match      41.0%; Score 66; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 DAEFRHDSGYEV 12

RESULT 3
09UCD1      PRELIMINARY;      PRT;      28 AA.
ID 09UCD1:
AC 09UCD1:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vingo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RL J. Neurochem. 61:1965-1968(1993).
DR HSP; P05067; IAMB.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match      41.0%; Score 66; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 DAEFRHDSGYEV 12

RESULT 4
09UC9      PRELIMINARY;      PRT;      30 AA.
ID 09UC9:
AC 09UC9:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

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DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Beta-amyloid protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lelowski M., Levy E., Marques M.R., Frangione B.;
RA "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 30 AA; 3391 MW; FP4167ABD081160A CRC64;

Query Match      41.0%; Score 66; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 DAEFRHDSGYEV 12

RESULT 5
09UC3      PRELIMINARY;      PRT;      33 AA.
ID 09UC3:
AC 09UC3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vingo-Pelfrey C., Bach F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlosseacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 33 AA; 3674 MW; B1DEF2F4167ABD0 CRC64;

Query Match      41.0%; Score 66; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 1 DAEFRHDSGYEV 12

RESULT 6
016020      PRELIMINARY;      PRT;      82 AA.
ID 016020:
AC 016020:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B.; Rosenzweig R.; Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 41.0%; Score 66; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 18 DAEFRHDSGYEV 29

RESULT 7
ID 016019 PRELIMINARY; PRT; 82 AA.
AC 016019;
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B.; Rosenzweig R.; Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 41.0%; Score 66; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 18 DAEFRHDSGYEV 29

RESULT 8
ID 08JH58 PRELIMINARY; PRT; 113 AA.
AC 08JH58;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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DE Amyloid beta protein (Fragment).
OC Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinidae; Chelydridae; Chelydra.
OC NCBI_TaxID=134619;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L.; Chiu S.; Kennedy S.M.; Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; A4 APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 41.0%; Score 66; DB 13; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
DB 15 DAEFRHDSGYEV 26

RESULT 9
ID 093296 PRELIMINARY; PRT; 534 AA.
AC 093296;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amyloid protein (Fragment).
GN Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

Query Match 41.0%; Score 66; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12

```

Db 436 DAEFRHDSGYEV 447

RESULT 10

Q9PVL1 PRELIMINARY; PRT; 569 AA.

AC Q9PVL1; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 GN App.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 tells us about its function.";
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL: AF030341; AAF12698.1; -;
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C-membrane; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PROSITE: PS00319; A4_INTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 41.0%; Score 66; DB 13; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 DB 472 DAEFRHDSGYEV 483

RESULT 11

Q9DCJ8 PRELIMINARY; PRT; 695 AA.

AC Q9DCJ8; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289218; AAG00593.1; -;
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C-membrane; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF02177; A4_EXTRA; 1.

DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00066; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; P201BD02ABC86D95 CRC64;

Query Match 41.0%; Score 66; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 DB 597 DAEFRHDSGYEV 608

RESULT 12

Q9DCJ7 PRELIMINARY; PRT; 751 AA.

AC Q9DCJ7; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289219; AAG00594.1; -;
 DR HSSP: P05067; 1BA4.
 DR GO: GO:0016020; C-membrane; IEA.
 DR GO: GO:004867; F-serine protease inhibitor activity; IEA.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 MW; E78B9413A033D84 CRC64;

Query Match 41.0%; Score 66; DB 13; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEV 12
 |||||
 DB 653 DAEFRHDSGYEV 664

RESULT 13

Q66147 PRELIMINARY; PRT; 552 AA.

AC Q66147; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Fusion protein precursor.
 OS Cetacean morbillivirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=36410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Porpoise;
 RX MEDLINE=95159670; PubMed=7531923;
 RA Bolt G.G.B., Blixenkron-Moller M.M.B., Gottschalk E., Wishaup R.G.,
 RA Welsh M.J., Earle J.A.P., Rima B.K.;
 RT "Nucleotide and deduced amino acid sequences of the matrix (M) and
 RT fusion (F) protein genes of cetacean morbilliviruses isolated from a
 RT porpoise and a dolphin."
 RL Virus Res. 34:291-304(1994).
 DR EMBL; X80757; CAA56731.1; -.
 DR PIR; S47034; S47034.
 DR HSSP; P04849; 1SVF.
 DR GO; GO:0019039; P:Viral-cell fusion molecule activity; IEA.
 DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; Fusion_gly.
 DR Pfam; PF00523; fusion_gly; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 552 AA; 60025 MW; 40D9191AD910EA1E CRC64;

Query Match 40.1%; Score 64.5; DB 12; Length 552;
 Best Local Similarity 44.8%; Pred. No. 0.8;
 Matches 13; Conservative 7; Mismatches 4; Indels 5; Gaps 1;

OY 9 GYEVKISI-----TEIKGVVHRIETLIF 32

DB 278 GYFIVLSIAVPTLSKVGIVHKLAVSY 306

RESULT 14
 Q66409 PRELIMINARY; PRT; 552 AA.
 AC Q66409;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Envelope glycoprotein.
 GN F.
 OS Dolphin morbillivirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=37131;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95159670; PubMed=7531923;
 RA Bolt G.G.B., Blixenkron-Moller M.M.B., Gottschalk E., Wishaup R.G.,
 RA Welsh M.J., Earle J.A.P., Rima B.K.;
 RT "Nucleotide and deduced amino acid sequences of the matrix (M) and
 RT fusion (F) protein genes of cetacean morbilliviruses isolated from a
 RT porpoise and a dolphin."
 RL Virus Res. 34:291-304(1994).
 DR EMBL; Z30086; CAA82903.1; -.
 DR HSSP; P04849; 1SVF.
 DR GO; GO:0019039; P:Viral-cell fusion molecule activity; IEA.
 DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; Fusion_gly.
 DR Pfam; PF00523; fusion_gly; 1.
 SQ SEQUENCE 552 AA; 59869 MW; 40298B33C392ADCD CRC64;

Query Match 38.2%; Score 61.5; DB 12; Length 552;
 Best Local Similarity 41.4%; Pred. No. 2.2;
 Matches 12; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

OY 9 GYEVKISI-----TEIKGVVHRIETLIF 32

DB 278 GYFIVLSIAVPTLSKVGIVHKLAVSY 306

RESULT 15
 ID 056852 PRELIMINARY; PRT; 552 AA.
 AC 056852;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE F protein.
 OS Dolphin morbillivirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=37131;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D15a from;
 RA Soethout E., Harder T.C., Osterhaus A.D.M.E.;
 RT "Expression of dolphin morbillivirus F and H genes in vaccinia virus."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ224704; CAA12077.1; -.
 DR HSSP; P04849; 1SVF.
 DR GO; GO:0019039; P:Viral-cell fusion molecule activity; IEA.
 DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; Fusion_gly.
 DR Pfam; PF00523; fusion_gly; 1.
 SQ SEQUENCE 552 AA; 59770 MW; 80F6A0F25AF3589 CRC64;

Query Match 38.2%; Score 61.5; DB 12; Length 552;
 Best Local Similarity 41.4%; Pred. No. 2.2;
 Matches 12; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

OY 9 GYEVKISI-----TEIKGVVHRIETLIF 32

DB 278 GYFIVLSIAVPTLSKVGIVHKLAVSY 306

Search completed: June 18, 2004, 20:02:29
 Job time : 32.0184 secs

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OM protein - protein search, using SW model

Run on: June 18, 2004, 19:49:20 ; Search time 49.0184 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-73

Perfect score: 177
Sequence: 1 DAEPFRDSEYVHKISITIKGVVRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	177	100.0	34 6	AAE35679 Human Abe
2	163	92.1	34 6	AAE35681 Human Abe
3	160	90.4	48 6	AAE35680 Human Abe
4	156	88.1	34 6	AAE35682 Human Abe
5	150	84.7	32 6	AAE35678 Human Abe
6	140	79.1	30 6	AAE35677 Human Abe
7	90	50.8	19 6	AAE35657 Human Abe
8	90	50.8	31 7	ADD89946 CD4 pep1
9	90	50.8	45 7	ADD89951 IGR pep1
10	90	50.8	50 7	ADD89944 CD4 pep1
11	89.5	50.6	35 2	AAW02335 Beta-amy1
12	89.5	50.6	35 2	AAW89355 Beta-amy1
13	89.5	50.6	35 5	ABG71015 Long form
14	89.5	50.6	35 5	ABW05163 Beta amy1
15	89	50.3	63 7	ADB33538 APP regio
16	89	50.3	63 7	ADB33537 APP regio
17	89	50.3	783 7	ADB33505 Human APP
18	89	50.3	783 7	ADB33503 Human APP
19	89	50.3	941 7	ADB33507 Human APP
20	89	50.3	941 7	ADB33509 Human APP
21	88.5	50.0	41 2	AAK45230 Beta amy1
22	88	49.7	26 7	ADB36573 APP epit
23	88	49.7	798 4	ABG19088 Novel hum
24	87.5	49.4	35 2	AAW89360 Beta-amy1
25	87	49.2	40 5	AAO18462 Human bet

26	87	49.2	42 5	AAO18463 Human bet
27	87	49.2	65 7	ADD89953 Foot-and
28	86	48.6	35 2	AAW89359 Beta-amy1
29	85.5	48.3	41 2	AAE22206 Alzheimer
30	85	48.0	51 2	AAW53984 Human ALZ
31	85	48.0	100 5	AAE14375 Amyloid p
32	85	48.0	108 5	AAE14383 Gamma-sec
33	85	48.0	112 2	AAE93556 Familial
34	85	48.0	162 1	AAE83151 Deduced s
35	85	48.0	162 2	AAE10023 Beta-amy1
36	85	48.0	162 2	AAE37863 Deduced f
37	85	48.0	695 2	AAE05166 Sequence
38	85	48.0	695 2	AAE19484 APP695 mu
39	85	48.0	695 3	AAW19498 APP695 ml
40	85	48.0	695 3	AAE8436 Human APP
41	85	48.0	695 4	AAU07207 Human bet
42	85	48.0	695 4	AAE10634 Human amy
43	85	48.0	695 4	AAE06864 Human amy
44	85	48.0	695 4	AAE02586 Human amy
45	85	48.0	695 4	AAU06608 Human Amy

ALIGNMENTS

RESULT 1	AAE35679	standard; peptide; 34 AA.
ID	AAE35679	
XX	AAE35679;	
AC		
XX		
DT	23-OCT-2003 (revised)	
DT	17-JUN-2003 (first entry)	
XX		
DE	Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.	
KW	Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease; Abeta; AD; brain tissue plaque; immunoneutralization; neuroprotective;	
KW	vaccine; neurotropic; human; hepatitis B virus; HBV; fusion peptide.	
XX		
OS	Homo sapiens.	
OS	Measles virus.	
OS	Chimeric.	
XX		
FT	Key	Location/Qualifiers
FT	Region	1..14
FT	Region	/note= "Human beta amyloid peptide"
FT	Region	18..34
FT	Region	/note= "Measles virus T helper cell epitope"
XX		
XX	WO200296350-A2.	
XX		
XX	05-DEC-2002.	
XX		
XX	02-APR-2002; 2002WO-US010293.	
XX		
XX	25-MAY-2001; 2001US-00865294.	
XX		
XX	(UNBI-) UNITED BIOMEDICAL INC.	
XX		
XX	Wang CY;	
XX		
XX	WPI; 2003-201258/19.	
XX		
XX	Novel peptide immunogen comprising a helper T cell epitope, an N-terminal	
XX	fragment of amyloid beta peptide linked to the epitope, and optionally a	
XX	spacer, useful for preventing or treating Alzheimer's disease.	
XX		
XX	Claim 9; Page 39; 77pp; English.	
XX		
XX	The present invention relates to a novel peptide immunogen comprising a	
XX	helper T cell (Th) epitope, an N-terminal fragment of amyloid beta	
XX	(Abeta) peptide (residues 1-42) linked to the epitope and optionally a	

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-Oct-2003 to standardise OS field)

SQ Sequence 34 AA;

Query Match 100.0%; Score 177; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHKISTEIKGVIVRIETTLF 34
DB 1 DAEFRHDSGYEVHHKISTEIKGVIVRIETTLF 34

RESULT 2

ID AAB35681 standard; peptide; 34 AA.

AC AAB35681;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.

XX Immunogen; helper T cell, Th epitope; amyloid beta; Alzheimer's disease;

XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;

XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

OS Homo sapiens.

OS Measles virus.

OS Chimeric.

OS Key

FH Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

Location/Qualifiers

1..14

/note="Human beta amyloid peptide"

18..34

/note="Measles virus T helper cell epitope"

WO200296350-A2.

05-DEC-2002.

02-APR-2002; 2002WO-US010293.

25-MAY-2001; 2001US-00865294.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI; 2003-201258/19.

Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

Disclosure; Page 39; 77pp; English.

The present invention relates to a novel peptide immunogen comprising a

CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-Oct-2003 to standardise OS field)

SQ Sequence 34 AA;

Query Match 92.1%; Score 163; DB 6; Length 34;
Best Local Similarity 91.2%; Pred. No. 6.4e-18;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHKISTEIKGVIVRIETTLF 34
DB 1 DAEFRHDSGYEVHHKISTEIKGVIVRIETTLF 34

RESULT 3

ID AAB35680 standard; peptide; 48 AA.

AC AAB35680;

DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.

XX Immunogen; helper T cell, Th epitope; amyloid beta; Alzheimer's disease;

XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;

XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

OS Homo sapiens.

OS Measles virus.

OS Chimeric.

OS Key

FH Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

Location/Qualifiers

1..28

/note="Human beta amyloid peptide"

32..48

/note="Measles virus T helper cell epitope"

WO200296350-A2.

05-DEC-2002.

02-APR-2002; 2002WO-US010293.

25-MAY-2001; 2001US-00865294.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI; 2003-201258/19.

Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

Disclosure; Page 39; 77pp; English.

Claim 9; Page 39; 77pp; English.

The present invention relates to a novel peptide immunogen comprising a

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (updated on 23-Oct-2003 to standardise OS field)

XX Sequence 48 AA:

Query Match 90.4%; Score 160; DB 6; Length 48;
Best Local Similarity 70.8%; Pred. No. 2.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 DAEFRHDSGYEVH-----KISTEIKGVYHRIETILF 34
DB 1 DAEFRHDSGYEVHOKLVFPADVDGSKISTEIKGVYHRIETILF 48

RESULT 4

AAE35682
ID AAE35682 standard; peptide; 34 AA.

XX AAE35682;

AC 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..14
FT /note= "Human beta amyloid peptide"

FT Region 18..34
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002MO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL, INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

XX PS Disclosure; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (updated on 23-Oct-2003 to standardise OS field)

XX Sequence 34 AA:

Query Match 88.1%; Score 156; DB 6; Length 34;
Best Local Similarity 91.2%; Pred. No. 7.8e-17;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHKKISTEIKGVYHRIETILF 34
DB 1 DAEFRHDSGYEVHKKISTEIKGVYHRIETILF 34

RESULT 5

AAE35678
ID AAE35678 standard; peptide; 32 AA.

XX AAE35678;

AC 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..12
FT /note= "Human beta amyloid peptide"

FT Region 16..32
FT /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002MO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL, INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal

PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

PS Claim 9, Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 32 AA:

Query Match 84.7%; Score 150; DB 6; Length 32;
Best Local Similarity 94.1%; Pred. No. 6.2e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYVHNKISTEIKGVIVHRIETILF 34
DB 1 DAEFRHDSGYV---KISTEIKGVIVHRIETILF 32

RESULT 6

AAE35677
ID AAE35677 standard; peptide; 30 AA.

AC AAE35677;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)

DB Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.
OS Measles virus.
OS Chimeric.

XX Key Location/Qualifiers
FT 1..10 "Human beta amyloid peptide"
FT Region 14..30
FT /note= "Measles virus T helper cell epitope"

XX MO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9, Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 30 AA:

Query Match 79.1%; Score 140; DB 6; Length 30;
Best Local Similarity 88.2%; Pred. No. 2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 DAEFRHDSGYVHNKISTEIKGVIVHRIETILF 34
DB 1 DAEFRHDSGY----KISTEIKGVIVHRIETILF 30

RESULT 7

AAE35657
ID AAE35657 standard; peptide; 19 AA.

AC AAE35657;
XX
DT 17-JUN-2003 (first entry)

DB Measles virus T helper cell epitope #31.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic.

XX Measles virus.
OS Measles virus.

XX MO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 1, Page 37; 77pp; English.

CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (A-beta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to A-beta
CC peptide that is cross-reactive to soluble A-beta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the A-beta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble A-beta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble A-beta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention
CC
CC Sequence 19 AA:

Query Match 50.8%; Score 90; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ISITIKGVIVRIETILF 34
Db 1 ISITIKGVIVRIETILF 19

RESULT 9
ADD89946
ID ADD89946 standard; protein; 31 AA.

AC ADD89946;

DT 29-JAN-2004 (first entry)

DE CD4 peptide used in immunostimulant complex for anti-HIV vaccine.

XX Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 20 /note= "Epsilon-lysine"

PN MO2003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

PS WPI; 2003-778890/73.

DR Stabilized immunostimulating complex, useful for vaccination, e.g.

PT against human immune deficiency viruses, comprises cationic peptide

XX immunogen and anionic oligonucleotide.

XX Claim 14; SEQ ID NO 6; 159pp; English.

XX The present sequence is that of a synthetic immunogenic peptide derived

CC from human CD4. This is an example of peptides that can be used in

CC claimed immunostimulatory complexes of the invention that are

CC specifically adapted to act as adjuvant and as peptide immunogen

CC stabiliser. The complexes comprise a Cpg oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to Cpg oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present CD4 derived peptide can be used in an anti
CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
XX Sequence 31 AA:

Query Match 50.8%; Score 90; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ISITIKGVIVRIETILF 34
Db 1 ISITIKGVIVRIETILF 19

RESULT 9
ADD89951
ID ADD89951 standard; protein; 45 AA.

AC ADD89951;

DT 29-JAN-2004 (first entry)

DE IGB peptide used in immunostimulant complex for allergy vaccine.

XX Immunostimulant; vaccine; human; immunogen; IGB; immunotherapy; allergy;

XX antibody; antiallergic.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 20 /note= "Epsilon-lysine"

PN MO2003068169-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004711.

PR 14-FEB-2002; 2002US-00076674.

PR 31-JAN-2003; 2003US-00076674.

XX (UNBI-) UNITED BIOMEDICAL INC.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Sokoll KK;

PS WPI; 2003-778890/73.

DR Stabilized immunostimulating complex, useful for vaccination, e.g.

PT against human immune deficiency viruses, comprises cationic peptide

XX immunogen and anionic oligonucleotide.

XX Claim 20; SEQ ID NO 11; 159pp; English.

XX The present sequence is that of a synthetic immunogenic peptide derived

CC from human IGB. This is an example of peptides that can be used in

CC claimed immunostimulatory complexes of the invention that are

CC specifically adapted to act as adjuvant and as peptide immunogen

CC stabiliser. The complexes comprise a Cpg oligonucleotide and a

CC biologically active peptide immunogen. The complex is particulate and can

CC efficiently present peptide immunogens to the cells of the immune system

CC to produce an immune response. The complexes may be prepared with various

CC ratios of peptides to Cpg oligonucleotides to provide different physical

CC properties, such as the size of the microparticle. An immunostimulatory

CC complex comprising the present IGB derived peptide can be used in an anti

CC -IGB immunotherapeutic vaccine for the treatment of allergy.

XX Sequence 45 AA;
SO Query Match 50.8%; Score 90; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16 ISITIKGVIVRIETILF 34
DB 1 ISITIKGVIVRIETILF 19
RESULT 10
ADDB9944
ID ADD89944 standard; protein; 50 AA.
XX AC ADD89944;
XX DT 29-JAN-2004 (first entry)
XX DB CD4 peptide used in immunostimulant complex as anti-HIV vaccine.
XX KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX MN W02003068169-A2.
XX PD 21-AUG-2003.
XX PF 14-FEB-2003; 2003WO-US004711.
XX PR 14-FEB-2002; 2002US-00076674.
XX PR 31-JAN-2003; 2003US-00076674.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI S0K01 KK;
XX DR WPI; 2003-778890/73.
XX PT Stabilized immunostimulating complex, useful for vaccination, e.g.
XX PT against human immune deficiency viruses, comprises cationic peptide
XX PT immunogen and anionic oligonucleotide.
XX PS Claim 14; SEQ ID NO 4; 159pp; English.
XX CC The present sequence is that of a synthetic immunogenic peptide derived
XX CC from human CD4. This is an example of peptides that can be used in
XX CC claimed immunostimulatory complexes of the invention that are
XX CC specifically adapted to act as adjuvant and as peptide immunogen
XX CC stabiliser. The complexes comprise a CPG oligonucleotide and a
XX CC biologically active peptide immunogen. The complex is particulate and can
XX CC efficiently present peptide immunogens to the cells of the immune system
XX CC to produce an immune response. The complexes may be prepared with various
XX CC ratios of peptides to CPG oligonucleotides to provide different physical
XX CC properties, such as the size of the microparticle. An immunostimulatory
XX CC complex comprising the present CD4 derived peptide can be used in an anti
XX CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX SO Sequence 50 AA;
Query Match 50.8%; Score 90; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16 ISITIKGVIVRIETILF 34
|||||

DB 1 ISITIKGVIVRIETILF 19
RESULT 11
ID AAM02335
XX AAM02335 standard; peptide; 35 AA.
XX AC AAM02335;
XX DT 06-MAY-1997 (first entry)
XX DB Beta-amyloid peptide residues 1-20, 26-40.
XX KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
XX KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
XX KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
XX KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
XX KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
XX KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
XX KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN W09628471-A1.
XX PD 19-SEP-1996.
XX PF 14-MAR-1996; 96WO-US003492.
XX PR 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PA (PHAR-) PHARM PEPTIDES INC.
XX PI Findeis MA, Benjamin H, Garnick MB, Gelfer M, Hundal A;
XX PI Kasman L, Musso G, Siger ER, Wakefield J, Reed MJ, Molineaux S;
XX PI Kubasek W, Chin J, Lee J, Kelley M;
XX DR WPI; 1996-433762/43.
XX PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
XX PT protein coupled (in)directly to at least 1 modifying gp., useful in
XX PT treatment of Alzheimer's disease.
XX PS Claim 29; Page 82; 106pp; English.
XX CC AAM02333-W02336 represent beta-amyloid peptide fragments that can be used
XX CC in the modulator compounds of the invention. Beta-amyloid peptide is a 4
XX CC kilodalton peptide that is the major protein component of amyloid
XX CC plaques. Amyloid plaques are present both in the brain lesions, and in
XX CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
XX CC amyloid modulators of the invention comprise an amyloidogenic protein or
XX CC peptide (see AAM02310-W02336) coupled directly or indirectly to at least
XX CC one modifying group. The modifying group is preferably a cyclic,
XX CC heterocyclic, or polycyclic group, such as decalin, a cholanlyl group, a
XX CC biotin containing group, or a fluorescein containing group. These
XX CC compounds then modulate the aggregation of these sequences to natural
XX CC amyloid proteins or peptides when contacted with the natural
XX CC amyloidogenic proteins or peptides. The modulator compounds can be used
XX CC in the treatment of disorders associated with amyloidosis, such as
XX CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
XX CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
XX CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
XX CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
XX CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
XX CC and other types of amyloidosis. The modulators are also useful for the
XX CC treatment of disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease
XX SO Sequence 35 AA;
Query Match 50.6%; Score 89.5; DB 2; Length 35;
|||||

Best Local Similarity 66.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 DAEFRHDSGYEVHH-KISTITIKGVIV 26
DB 1 DAEFRHDSGYEVHHQKLVFPFNKGAII 27

RESULT 12

AAW89355
ID AAW89355 standard; peptide; 35 AA.

AC AAW89355;

DT 02-MAR-1999 (first entry)

DE Beta-amyloid peptide derivative A-beta-1-20,26-40.

XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;

KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

KM familial amyloid polynuropathy; bovine spongiform encephalopathy;

KM Creutzfeldt-Jakob disease; BAP.

XX Homo sapiens.

OS Synthetic.

XX US8554204-A.

PD 29-DEC-1998.

XX 14-MAR-1996; 96US-00612785.

PR 14-MAR-1995; 95US-00404831.

PR 07-JUN-1995; 95US-00475579.

PR 27-OCT-1995; 95US-00548998.

XX (PRAB-) PRACIS PHARM INC.

PI Hundal A, Gelfer ML, Kasman L, Musco G, Molineux S, Benjamin H;

PI Findeis MA, Chin J, Lee J, Kelley W, Reed M, Wakefield J;

PI Garrick MB, Kubaek W, Signer ER;

XX MPI; 1999-094964/08.

XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid

PT aggregation - and neurotoxicity, specifically for treatment and

PT prevention of Alzheimer's disease.

PS Claim 3; Col 71-72; 52pp; English.

XX The present invention describes beta-amyloid peptide (BAP) derivatives.

CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and

CC peptides, specifically BAP, and their neurotoxicity, so are useful for

CC treating and preventing any disease involving amyloidosis, specifically

CC Alzheimer's disease but also Down's syndrome, familial amyloid

CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and

CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose

CC these diseases, in vitro or in vivo, by detecting binding of BAP to

CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation

CC even when BAP is present in molar excess. The present sequence represents

CC a BAP derivative

XX Sequence 35 AA;

Query Match 50.6%; Score 89.5; DB 2; Length 35;

Best Local Similarity 66.7%; Pred. No. 1.8e-06;

Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 DAEFRHDSGYEVHH-KISTITIKGVIV 26

DB 1 DAEFRHDSGYEVHHQKLVFPFNKGAII 27

RESULT 13

ABG71015
ID ABG71015 standard; peptide; 35 AA.

AC ABG71015;

DT 05-DEC-2002 (first entry)

DE Long form beta-amyloid protein fragment, mutant #2.

XX Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;

KM familial amyloid polynuropathy; familial amyloid cardiomyopathy;

KM isolated cardiac amyloid; systemic senile amyloidosis; scarpie; myeloma;

KM bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;

KM adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;

KM insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;

KM macroglobulinaemia-associated amyloidosis; reactive amyloidosis;

KM primary localized cutaneous nodular amyloidosis; Sjogren's syndrome;

KM hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;

KM hereditary non-neuropathic systemic amyloidosis;

XX familial Mediterranean Fever; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

XX Misc-difference 1..20 of Beta-amyloid (ABG71001) "

XX Misc-difference 21..35

XX /note="Residues 26-40 of beta-amyloid (ABG71001) "

XX US2002098173-A1.

XX 25-JUL-2002.

XX 04-OCT-2001; 2001US-00972475.

XX 14-MAR-1995; 95US-00404831.

XX 07-JUN-1995; 95US-00475579.

XX 27-OCT-1995; 95US-00548998.

XX 14-MAR-1996; 96US-00617267.

XX (PRAB-) PRACIS PHARM INC.

XX Findeis MA, Benjamin H, Garrick MB, Gelfer ML, Hundal A;

XX Kasman L, Musco G, Signer ER, Wakefield J, Reed MJ;

XX MPI; 2002-697709/75.

XX Amyloid modulator useful for treating a disorder associated with

XX amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment

XX coupled to a modifying group.

XX Example 12; Page; 41pp; English.

XX The invention describes an amyloid modulator comprising an amyloidogenic

XX protein and/or peptide fragment coupled to a modifying group so that the

XX compound modulates the aggregation of natural amyloid proteins or

XX peptides. The modulator is used for treating a disorder associated with

XX amyloidosis e.g. familial amyloid polynuropathy (Portuguese, Japanese

XX and Swedish types), familial amyloid cardiomyopathy (Danish type),

XX isolated cardiac amyloid, systemic senile amyloidosis, scarpie, bovine

XX spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset

XX diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated

XX atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or

XX macroglobulinaemia-associated amyloidosis, primary localized cutaneous

XX nodular amyloidosis associated with Sjogren's syndrome, reactive

XX (secondary) amyloidosis, familial Mediterranean Fever and familial

XX amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),

XX hereditary cerebral haemorrhage with amyloidosis of Icelandic type,

XX amyloidosis associated with long term haemodialysis, hereditary non-

XX neuropathic systemic amyloidosis (familial amyloid polynuropathy III),

XX familial amyloidosis of Finnish type, amyloidosis associated with

CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
CC renal amyloidosis and lysosome-associated hereditary systemic
CC amyloidosis. The compound is capable of altering and inhibiting beta-
CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents a mutant of the long
CC form of beta-amyloid used in the creation of an amyloid modulator. Note:
CC This sequence does not appear in the specification but has been created
CC from the wild type sequence (ABG71001) using information given in the
CC invention

XX
XX
SQ Sequence 35 AA;

Query Match 50.6%; Score 89.5; DB 5; Length 35;
Best Local Similarity 66.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DAERFHDGVEVHH-KISTEIKGVIV 26
Db 1 DAERFHDGVEVHHQKLVFNSKGAII 27

RESULT 14

ABB05163 ID ABB05163 standard; peptide; 35 AA.

AC ABB05163;

DT 02-APR-2002 (first entry)

DE Beta amyloid peptide (1-20,26-40) SEQ ID NO:15.

XX Beta amyloid peptide; beta-AP, beta amyloid precursor protein; A-beta;
XX APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
XX neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
XX antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
XX amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
XX amyloidogenic disease; beta amyloid deposition; amyloidosis;
XX hereditary cerebral haemorrhage; familial amyloid polyneuropathy.

OS Homo sapiens.
OS Synthetic.

PN US6319498-B1.

PD 20-NOV-2001.

PF 14-MAR-1996; 96US-00617267.

PR 14-MAR-1995; 95US-00404831.

PR 07-JUN-1995; 95US-00475579.

PR 27-OCT-1995; 95US-00548998.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
PI Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-146668/19.

XX Amyloid modulator compound useful for treatment of an amyloidogenic
PT disease such as Alzheimer's disease comprises an aggregation core domain
PT and a modifying group attached to it.

XX Disclosure; Col 75; 54pp; English.

XX The present invention describes an amyloid modulator compound (I)
CC comprising an aggregation core domain and a modifying group attached to
CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
CC and auditory activities, and can be used as a natural amyloid aggregation
CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
CC (beta-AP). (I) are used in the manufacture of a medicament for the

CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
CC disease and other clinical occurrences of beta amyloid deposition such as
CC Down's syndrome, individuals and in patients with hereditary cerebral
CC haemorrhage with amyloidosis, and for treating a disorder associated with
CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the
CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
CC not only reduces the formation of neurotoxic aggregates but also have the
CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
CC present sequence represents a beta-AP peptide, which is used in the
CC exemplification of the present invention

XX
XX
SQ Sequence 35 AA;

Query Match 50.6%; Score 89.5; DB 5; Length 35;
Best Local Similarity 66.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DAERFHDGVEVHH-KISTEIKGVIV 26
Db 1 DAERFHDGVEVHHQKLVFNSKGAII 27

RESULT 15

ADB33538 ID ADB33538 standard; protein; 63 AA.

AC ADB33538;

DT 04-DEC-2003 (first entry)

DE APP region SEQ ID NO:37.

XX fusion protein; amyloid precursor protein; APP; transcription factor;
XX neurotropic; neuroprotective; APP inhibitor;
XX amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase;
XX gamma-secretase; human.

XX Synthetic.

OS Homo sapiens.

PN WO2003072041-A2.

PD 04-SEP-2003.

PF 23-FEB-2003; 2003WO-US005458.

PR 27-FEB-2002; 2002US-0360274P.

XX (MERI) MERCK & CO INC.

XX Espeseth AS, Ferrer M, Flores OA, Hazuda DJ, Inglese J;
PI Miller MD, Register B, Shi X, Simon MJ, Zuck PD;

XX WPI; 2003-689968/65.

XX DNA encoding a fusion protein of amyloid precursor protein, useful in
PT screening for anti-Alzheimer agents, comprises a fused transcription
PT factor.

XX Disclosure; Page 18; 193pp; English.

XX The present invention describes a DNA molecule (I) that encodes a fusion
CC protein (PP) comprising: (i) an amino acid sequence of amyloid precursor
CC protein (APP), either the wild type, Swedish or NFEV versions; and (ii) a
CC transcription factor (TF), fused in frame to the C-terminus of (i). Also
CC described: (1) an expression vector containing (I); (2) a eukaryotic cell
CC containing (I); and (3) methods for identifying a compound (A) that
CC inhibits processing of APP, using the cells of (2). (I) has neurotropic and
CC neuroprotective activities. (I) can be used to produce eukaryotic cells
CC that express PP and are useful in screening for agents that inhibit
CC processing of APP. The agents are potentially useful for the treatment or
CC prevention of Alzheimer's disease. Cells that express PP can screen for
CC inhibitors of: (a) beta- and gamma-secretase; and (b)

CC cytoplasmic/extracellular APP signaling in a single assay. Cell-based
 CC assays may be free of interference from alpha-secretase activity and are
 CC homogeneous (no chromatography, immunoprecipitation or washing required)
 CC so well suited to high-throughput screening. The present sequence
 CC represents a human APP amino acid sequence, which is given in the
 CC exemplification of the present invention.

XX
 SQ Sequence 63 AA;

Query Match 50.3%; Score 89; DB 7; Length 63;
 Best Local Similarity 53.1%; Pred. No. 4.5e-06;
 Matches 17; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

QY 1 DAEFRHDSGYGVHKKI-----SITEIKGVIV 26
 DB 9 DAEFRHDSGYGVHKKI-----SITEIKGVIV 40

Search completed: June 18, 2004, 19:58:52
 Job time : 50.0184 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 18, 2004, 19:54:46 ; Search time 13.3497 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-73

Sequence: 1 DAFRRDGGVHVKISITFKGVVRIETILF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTCUTS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	89.5	50.6	35 2 US-08-612-785B-15	Sequence 15, Appl
2	89.5	50.6	35 4 US-08-617-267C-15	Sequence 15, Appl
3	87.5	49.4	35 2 US-08-612-785B-39	Sequence 39, Appl
4	86	48.6	35 2 US-08-612-785B-38	Sequence 38, Appl
5	85.5	48.3	41 1 US-07-819-361-1	Sequence 1, Appl
6	85	48.0	38 6 526232-1	Patent No. 526232
7	85	48.0	152 6 5187153-4	Patent No. 5187153
8	85	48.0	152 6 5220013-4	Patent No. 5220013
9	85	48.0	152 6 5223482-4	Patent No. 5223482
10	85	48.0	635 4 US-09-548-372D-14	Sequence 14, Appl
11	85	48.0	635 4 US-09-548-367D-14	Sequence 14, Appl
12	85	48.0	635 4 US-09-551-853D-14	Sequence 14, Appl
13	85	48.0	637 4 US-09-548-372D-20	Sequence 20, Appl
14	85	48.0	637 4 US-09-548-367D-20	Sequence 20, Appl
15	85	48.0	637 4 US-09-551-853D-20	Sequence 20, Appl
16	84.5	47.7	42 1 US-08-268-348A-6	Sequence 6, Appl
17	84	47.5	43 2 US-08-404-831-3	Sequence 3, Appl
18	84	47.5	43 2 US-08-612-785B-3	Sequence 3, Appl
19	84	47.5	43 2 US-08-475-579A-3	Sequence 3, Appl
20	84	47.5	43 4 US-08-617-267C-3	Sequence 3, Appl
21	83	46.9	15 2 US-08-609-090-1	Sequence 1, Appl
22	83	46.9	16 1 US-08-302-808-10	Sequence 10, Appl
23	83	46.9	16 2 US-08-386-948-10	Sequence 10, Appl
24	83	46.9	17 4 US-09-594-366-2	Sequence 2, Appl
25	83	46.9	21 2 US-08-659-984A-18	Sequence 18, Appl
26	83	46.9	21 3 US-08-660-531-18	Sequence 18, Appl
27	83	46.9	27 1 US-08-141-324-11	Sequence 11, Appl

28	83	46.9	27 1 US-08-141-324-12	Sequence 12, Appl
29	83	46.9	27 1 US-08-541-902-11	Sequence 11, Appl
30	83	46.9	27 1 US-08-541-902-12	Sequence 12, Appl
31	83	46.9	28 1 US-08-346-849-4	Sequence 4, Appl
32	83	46.9	28 1 US-08-302-808-7	Sequence 7, Appl
33	83	46.9	28 2 US-08-609-090-2	Sequence 2, Appl
34	83	46.9	28 2 US-08-986-948-7	Sequence 7, Appl
35	83	46.9	28 2 US-08-293-284A-4	Sequence 4, Appl
36	83	46.9	28 2 US-08-461-216-2	Sequence 2, Appl
37	83	46.9	28 3 US-09-388-890-2	Sequence 2, Appl
38	83	46.9	28 3 US-09-388-890-11	Sequence 11, Appl
39	83	46.9	28 3 US-09-388-890-12	Sequence 12, Appl
40	83	46.9	28 3 US-09-388-890-13	Sequence 13, Appl
41	83	46.9	28 3 US-09-388-890-14	Sequence 14, Appl
42	83	46.9	28 4 US-08-723-661B-2	Sequence 2, Appl
43	83	46.9	28 4 US-09-660-954-2	Sequence 2, Appl
44	83	46.9	28 4 US-09-660-954-11	Sequence 11, Appl
45	83	46.9	28 4 US-09-660-954-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-612-785B-15
Sequence 15, Application US/08612785B

Patent No. 5854204

GENERAL INFORMATION:

APPLICANT: Findex, Mark A. et al.

TITLE OF INVENTION: AD Peptides that Modulate b-Amyloid

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHYE & COCKFIELD

STREET: 28 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,785B

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-612-785B-15

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA: USN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-612-785B-38

Query Match 48.6%; Score 86; DB 2; Length 35;
Best Local Similarity 63.0%; Pred. No. 8.9e-07;
Matches 17; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEVHKK--ISITIKGVI 25
DB 1 DAEFRHDSGYEVHKKLVFPAEDVGII 27

RESULT 5
US-07-819-361-1
Sequence 1, Application US/07819361
Patent No. 5338663
GENERAL INFORMATION:
APPLICANT: Potter, Huntington
APPLICANT: Kayyali, Usamah
TITLE OF INVENTION: Method of Interfering With Formation of
TITLE OF INVENTION: Alpha-Antichymotrypsin-Beta-Protein Complex, Method of
TITLE OF INVENTION: Inhibiting Beta-Protein Function and Compounds For Use
TITLE OF INVENTION: Therein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/819,361
FILING DATE: 19920113
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: H090-03A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-819-361-1

Query Match 48.3%; Score 85.5; DB 1; Length 41;
Best Local Similarity 54.8%; Pred. No. 1.3e-06;
Matches 17; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

OY 1 DAEFRHDSGYEVHKK-----ISITIKGVI 26
DB 1 DAEFRHDSGYEVHKKLVFPAEDVGNKCAII 31

RESULT 6
5262332-1
Patent No. 5262332
APPLICANT: SELKOE, DENNIS J.
TITLE OF INVENTION: DIAGNOSTIC METHOD FOR ALZHEIMER'S
DISEASE: EXAMINATION OF NON-NEURAL TISSUE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/410,138
FILING DATE: 19-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 333,609
FILING DATE: 05-APR-1989
SEQ ID NO: 1
LENGTH: 38
5262332-1

Query Match 48.0%; Score 85; DB 6; Length 38;
Best Local Similarity 69.6%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHKKISITIKG 23
DB 1 DAEFRHDSGYEVHKKLVFPAEDVG 23

RESULT 7
5187153-4
Patent No. 5187153
APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
AMYLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 4
LENGTH: 152
5187153-4

Query Match 48.0%; Score 85; DB 6; Length 152;
Best Local Similarity 71.4%; Pred. No. 8.2e-06;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAEFRDSDGYEVHKKISTEI 21
| | | | | | | | | | : : :
Db 74 DAEFRDSDGYEVHKKISTEI 94

RESULT 8
5220013-4
PATENT No. 5220013
APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/444,118
FILING DATE: 30-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO:4:
LENGTH: 162
5220013-4

Query Match 48.0%; Score 85; DB 6; Length 162;
Best Local Similarity 71.4%; Pred. No. 8.9e-06;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAEFRDSDGYEVHKKISTEI 21
| | | | | | | | | | : : :
Db 81 DAEFRDSDGYEVHKKISTEI 101

RESULT 9
5223482-4
PATENT No. 5223482
APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
BARBARA
TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/361,912
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO:4:
LENGTH: 162
5223482-4

Query Match 48.0%; Score 85; DB 6; Length 162;
Best Local Similarity 71.4%; Pred. No. 8.9e-06;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAEFRDSDGYEVHKKISTEI 21
| | | | | | | | | | : : :
Db 81 DAEFRDSDGYEVHKKISTEI 101

RESULT 10

US-09-548-372D-14
Sequence 14, Application US/09548372D
Patent No. 6420534

GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-14

Query Match 48.0%; Score 85; DB 4; Length 695;
Best Local Similarity 43.5%; Pred. No. 5.6e-05;
Matches 20; Conservative 5; Mismatches 9; Indels 12; Gaps 2;
QY 1 DAEFRDSDGYEVHKKISTEI 34
| | | | | | | | | | : : :
Db 597 DAEFRDSDGYEVHKKISTEI 642

RESULT 11
US-09-548-367D-14
Sequence 14, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,367D
FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-367D-14

Query Match 48.0%; Score 85; DB 4; Length 695;
Best Local Similarity 43.5%; Pred. No. 5.6e-05;
Matches 20; Conservative 5; Mismatches 9; Indels 12; Gaps 2;
QY 1 DAEFRDSDGYEVHKKISTEI 34
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Db 597 DAEFRDSDGYEVHKKISTEI 642

RESULT 12
US-09-551-853D-14

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: Sequence 14, Application US/09551853D
: Patent No. 6500667
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280L
: CURRENT APPLICATION NUMBER: US/09/551,853D
: CURRENT FILING DATE: 2000-04-18
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 695
: TYPE: PRY
: ORGANISM: Homo sapiens
: US-09-551-853D-14

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Query Match	48.0%	Score 85;	DB 4;	Length 695;
Best Local Similarity	43.5%	Pred. No. 5.6e-05;		
Matches	20;	Conservative	5;	Mismatches 9;
			Indels	12;
			Gaps	2;
Qy	1	DAEHRHDSQGVVHNR-----	ISTETIRGVVHNR-----	ITETILF 34
Db	597	DAEHRHDSQGVVHNRHOKLVFPADBDGNSKGAIIIGLMVGGVATATATVF		642

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RESULT 13
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-372D-20

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Query Match	48.0%;	Score	85;	DB	4;	Length	697;
Best Local	43.5%;	Pred	No.	5.6e-05;			
Matches	20;	Conservative	5;	Mismatches	9;	Indels	12;
						Gaps	2

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Oy      1 DAEPRDSCYEVAHK-----ISITEIKGVYHR-----IETILF 34
          |||||         :   |   |   |   |   |   |   |
Db      597 DAEFRHDSGEVHHQKLVFAEDVGSNKGALIGLWGSVIATVIP 642
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RESULT 14
US-09-548-367D-20
; Sequence 20, Application US/09548367D

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: Patent No. 6440698
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280H
: CURRENT APPLICATION NUMBER: US/09/548,367D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20081
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-548-367D-20

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Query Match      48.0%; SCORE 85; DB 4; Length 697;
Best Local Similarity 43.5%; Pred. No. 5.6e-05;
Matches 20; Conservative 5; Mismatches 9; Indels 12; Gaps 2

QY      1 DAERRHDSGYEVHKK-----ISTETKGVVHR-----LETLIF 34
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      597 DAERRHDSGYEVHKKQVFPFAEDGSSNKGALITGLMGCVTAIATVF 642

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RESULT 15
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551, 853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

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Query Match	48.0%	Score 85	DB 4	length 697
Best Local Similarity	43.5%	Pred. No.	5.6e-05	
Matches 20; Conservative	5	Mismatches	9	Indels 12; Gaps 2

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Oy      1 DAEFRDSCGYEVHMK-----ISITEIKGVIVHR-----ITETLP 34
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Db      597 DAEFRDSCGYEVHMKLVFAEDVGSNKGAIIGLMVGVIATVIP 6422

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Search completed: June 18, 2004, 20:04:46
Job time : 14.3497 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 38.3804 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294a-73

Perfect score: 177
Sequence: 1 DAFRRDSCGYVHKRISTEIKGVIHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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15: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
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2	163	92.1	34	10	US-09-865-294-75 Sequence 75, Appl
3	160	90.4	48	10	US-09-865-294-74 Sequence 74, Appl
4	156	88.1	34	10	US-09-865-294-76 Sequence 76, Appl
5	150	84.7	32	10	US-09-865-294-72 Sequence 72, Appl
6	140	79.1	30	10	US-09-865-294-71 Sequence 71, Appl
7	90	50.8	19	10	US-09-865-294-51 Sequence 51, Appl
8	90	50.8	31	14	US-10-076-674-6 Sequence 6, Appl
9	90	50.8	31	15	US-10-355-161A-6 Sequence 6, Appl
10	90	50.8	45	15	US-10-076-674-11 Sequence 11, Appl
11	90	50.8	45	15	US-10-355-161A-11 Sequence 11, Appl
12	90	50.8	50	14	US-10-076-674-4 Sequence 4, Appl
13	90	50.8	50	15	US-10-355-161A-4 Sequence 4, Appl
14	89.5	50.6	35	9	US-09-972-475-15 Sequence 15, Appl
15	89.5	50.6	35	15	US-10-463-729-15 Sequence 15, Appl

16	87	49.2	65	15	US-10-355-161A-13	Sequence 13, Appl
17	85	48.0	100	15	US-10-275-025-5	Sequence 5, Appl
18	85	48.0	108	15	US-10-275-025-13	Sequence 13, Appl
19	85	48.0	695	9	US-09-794-927-14	Sequence 14, Appl
20	85	48.0	695	9	US-09-795-847-14	Sequence 14, Appl
21	85	48.0	695	9	US-09-794-743-14	Sequence 14, Appl
22	85	48.0	695	9	US-09-794-748-14	Sequence 14, Appl
23	85	48.0	695	9	US-09-794-925-14	Sequence 14, Appl
24	85	48.0	695	9	US-09-681-442-14	Sequence 14, Appl
25	85	48.0	695	10	US-09-869-414-14	Sequence 14, Appl
26	85	48.0	695	10	US-09-548-366-14	Sequence 14, Appl
27	85	48.0	695	12	US-10-652-927-14	Sequence 14, Appl
28	85	48.0	695	12	US-10-652-830-14	Sequence 14, Appl
29	85	48.0	697	9	US-09-794-927-20	Sequence 20, Appl
30	85	48.0	697	9	US-09-795-847-20	Sequence 20, Appl
31	85	48.0	697	9	US-09-794-743-20	Sequence 20, Appl
32	85	48.0	697	9	US-09-794-748-20	Sequence 20, Appl
33	85	48.0	697	9	US-09-794-925-20	Sequence 20, Appl
34	85	48.0	697	9	US-09-681-442-20	Sequence 20, Appl
35	85	48.0	697	10	US-09-869-414-20	Sequence 20, Appl
36	85	48.0	697	10	US-09-548-366-20	Sequence 20, Appl
37	85	48.0	697	12	US-10-652-927-20	Sequence 20, Appl
38	85	48.0	697	12	US-10-652-830-20	Sequence 20, Appl
39	84	47.5	42	14	US-10-217-584-11	Sequence 11, Appl
40	84	47.5	43	9	US-09-972-475-3	Sequence 3, Appl
41	84	47.5	43	15	US-10-463-729-3	Sequence 3, Appl
42	83	46.9	16	9	US-09-155-076-2	Sequence 2, Appl
43	83	46.9	16	12	US-10-423-047-2	Sequence 2, Appl
44	83	46.9	16	15	US-10-411-544-22	Sequence 2, Appl
45	83	46.9	17	9	US-09-992-800-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US20030068325A1
GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-73

Query Match 100.0%; Score 177; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAFRRDSCGYVHKRISTEIKGVIHRIETILF 34
Db 1 DAFRRDSCGYVHKRISTEIKGVIHRIETILF 34

RESULT 2
US-09-865-294-75
; Sequence 75, Application US/09865294
; Publication No. US20030068325A1
GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

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/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 75
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Measles virus
US-09-865-294-75

Query Match          92.1%; Score 163; DB 10; Length 34;
Best Local Similarity 91.2%; Pred. No. 1.4e-16;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
DB 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34

RESULT 3
US-09-865-294-74
/ Sequence 74, Application US/09865294
/ Publication No. US20030068325A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
/ FILE REFERENCE: 1151-4167
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 74
/ LENGTH: 48
/ TYPE: PRT
/ ORGANISM: Measles virus
US-09-865-294-74

Query Match          90.4%; Score 160; DB 10; Length 48;
Best Local Similarity 70.8%; Pred. No. 5.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
DB 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 48

RESULT 4
US-09-865-294-76
/ Sequence 76, Application US/09865294
/ Publication No. US20030068325A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
/ FILE REFERENCE: 1151-4167
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 76
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Measles virus
US-09-865-294-76

Query Match          88.1%; Score 156; DB 10; Length 34;
Best Local Similarity 91.2%; Pred. No. 1.4e-15;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
DB 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
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RESULT 5
US-09-865-294-72
/ Sequence 72, Application US/09865294
/ Publication No. US20030068325A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
/ FILE REFERENCE: 1151-4167
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 72
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Measles virus
US-09-865-294-72

Query Match          84.7%; Score 150; DB 10; Length 32;
Best Local Similarity 94.1%; Pred. No. 1e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
DB 1 DAEFRHDSGYEV--KISTEIKGVVHRIETILF 32

RESULT 6
US-09-865-294-71
/ Sequence 71, Application US/09865294
/ Publication No. US20030068325A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
/ FILE REFERENCE: 1151-4167
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 71
/ LENGTH: 30
/ TYPE: PRT
/ ORGANISM: Measles virus
US-09-865-294-71

Query Match          79.1%; Score 140; DB 10; Length 30;
Best Local Similarity 88.2%; Pred. No. 2.7e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 DAEFRHDSGYEVHHKISTEIKGVVHRIETILF 34
DB 1 DAEFRHDSGYEV---KISTEIKGVVHRIETILF 30

RESULT 7
US-09-865-294-51
/ Sequence 51, Application US/09865294
/ Publication No. US20030068325A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
/ FILE REFERENCE: 1151-4167
/ CURRENT FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 51
/ LENGTH: 19
/ TYPE: PRT
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ORGANISM: Measles virus
US-09-865-294-51

Query Match 50.8%; Score 90; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ISITEIKGVIVHRIETILF 34
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 8

US-10-076-674-6
; Sequence 6, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

Query Match 50.8%; Score 90; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ISITEIKGVIVHRIETILF 34
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 9

US-10-355-161A-6
; Sequence 6, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

Query Match 50.8%; Score 90; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ISITEIKGVIVHRIETILF 34
DB 1 ISITEIKGVIVHRIETILF 19

DB 1 ISITEIKGVIVHRIETILF 19

RESULT 10
US-10-076-674-11
; Sequence 11, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

Query Match 50.8%; Score 90; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ISITEIKGVIVHRIETILF 34
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 11
US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

Query Match 50.8%; Score 90; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ISITEIKGVIVHRIETILF 34
DB 1 ISITEIKGVIVHRIETILF 19

RESULT 12
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.

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; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc:feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

Query Match          50.8%; Score 90; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ISITEIKGVIVHRIETILP 34
      |||||
Db      1 ISITEIKGVIVHRIETILP 19

RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc:feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

Query Match          50.8%; Score 90; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ISITEIKGVIVHRIETILP 34
      |||||
Db      1 ISITEIKGVIVHRIETILP 19

RESULT 14
US-09-972-475-15
; Sequence 15, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-972-475-15

Query Match          50.6%; Score 89.5; DB 9; Length 35;
Best Local Similarity 66.7%; Pred. No. 7.6e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY      1 DAEFRHDSGYEVH-RKISITEIKGVIV 26
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Db      1 DAEFRHDSGYEVHQLVFPSSNKALII 27

RESULT 15
US-10-463-729-15
; Sequence 15, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/548,998
 FILING DATE: 27-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: PPI-002CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-10-463-729-15

Query Match 50.6%; Score 89.5; DB 15; Length 35;
 Best Local Similarity 66.7%; Pred. No. 7.6e-06;
 Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHH-KISTYIKGVIV 26
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 DB 1 DAEFRHDSGYEVHHQKLVFPSNKGATL 27

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 Job time: 38.3804 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 10.2209 Seconds

(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-73

Perfect score: 177
Sequence: 1 DAEPFRHDSGYEVHMKSTIEIKCVIARIITILP 34Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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7	83	46.9	57	2	B60045
8	83	46.9	82	2	F60048
9	83	46.9	695	1	A49795
10	83	46.9	770	1	QRHUA4
11	68	38.4	747	2	JH0773
12	64	36.2	33	2	S23094
13	64	36.2	546	1	VGNZRL
14	64	36.2	695	2	A27485
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16	61	34.5	546	2	S47300
17	60	33.9	546	1	VGNZKR
18	60	33.9	546	2	S55386
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21	59	33.3	552	2	S47034
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23	59	33.3	662	2	S21382
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27	58	32.8	550	1	R48556
28	58	32.8	553	1	VGNZMY
29	58	32.8	631	1	VGNZPD

30	58	32.8	631	1	A48346	cell fusion glycop
31	57.5	32.5	356	2	D96537	hypothetical prote
32	54.5	30.8	236	2	A80190	hypothetical prote
33	52	29.4	220	2	T90801	probable synaptob
34	52	29.4	229	2	F61800	hypothetical prote
35	51.5	29.1	539	2	T39150	probable heat shoc
36	51	28.8	239	2	T34305	hypothetical prote
37	51	28.8	240	2	T47589	synaptobrevin-like
38	51	28.8	854	2	D83077	C18B protein PA454
39	50.5	28.5	427	2	S38002	hypothetical prote
40	50.5	28.5	503	2	AB1933	hypothetical prote
41	50	28.2	605	2	G70409	high affinity sulf
42	49.5	28.0	367	2	C96537	hypothetical prote
43	49.5	28.0	615	2	A82025	probable outer mem
44	49.5	28.0	635	2	G81003	conserved hypothet
45	49.5	28.0	4563	1	LEHUB	apolipoprotein B-1

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimomigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, Y.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm

A:Reference number: PN0512; MUID:93290653; PMID:7685598

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid

Query Match 46.9%; Score 83; DB 2; Length 42;

Best Local Similarity 93.3%; Pred. No. 6e-05; Mismatches 0; Gaps 0;

Matches 14; Conservative 1; Indels 0;

QY 1 DAEPFRHDSGYEVHMK 15
DB 1 DAEPFRHDSGYEVHMQ 15

RESULT 2

B60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, P.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <J0H>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;

Best Local Similarity 93.3%; Pred. No. 8.4e-05; Mismatches 0; Gaps 0;

Matches 14; Conservative 1; Indels 0;

QY 1 DAEPFRHDSGYEVHMK 15
DB 6 DAEPFRHDSGYEVHMQ 20

RESULT 3

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C/Accession: F60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: F60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896
C/Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 6 DAEFRHDSGYEVHHQ 20

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: G60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: G60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56126
C/Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 6 DAEFRHDSGYEVHHQ 20

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: D60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: D60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56124
C/Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15

DB 6 DAEFRHDSGYEVHHQ 20

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: A60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: A60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56125
C/Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 6 DAEFRHDSGYEVHHQ 20

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C/Species: Ursus maritimus (polar bear)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C/Accession: B60045
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: B60045
A/Molecule type: mRNA
A/Residues: 1-57 <JOH>
A/Cross-references: EMBL:X56128; NID:92165; PIDN:CA39593.1; PID:92166
C/Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 6 DAEFRHDSGYEVHHQ 20

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C/Accession: PQ0438; C60045
R/Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A/Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A/Reference number: PQ0438; MUID:93075180; PMID:1445331
A/Accession: PQ0438
A/Molecule type: DNA
A/Residues: 1-82 <DAV>
A/Cross-references: GB:M83558; GB:M83657
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 46.9%; Score 83; DB 2; Length 82;
Best Local Similarity 93.3%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
Db 17 DAEFRHDSGYEVHHQ 31

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a R
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36629.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing

Query Match 46.9%; Score 83; DB 1; Length 695;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
Db 597 DAEFRHDSGYEVHHQ 611

RESULT 10
Q8R0U4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N:Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33600; A3486; I39452; I39451; I39453; I59562; A44
4688; A28883; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R:LeMayre, H.G.; Salbaum, J.M.; Multhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PEA4(655) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:LeMayre, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA1830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:LeMayre, H.G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-proti
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LA>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAIC1654.1; PID:g516074
R:Johnson, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similar
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:g178863; PIDN:AA51768.1; PID:g178865
R:Prelli, F.; Levy, B.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRB1>
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90263618; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
A:Residues: 1-770 <YOS1>
A:Molecule type: DNA
A:Cross-references: GB:M33112; NID:g178613; PIDN:AA59502.1; PID:g178616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
A:Molecule type: DNA
A:Residues: 1-530, 'QWMPVTPAFAKVGK' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Accession: A59020
A:Contents: annotation; exatum
A:Note: revised physical map for reference I39451
R:Levy, B.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBU
A:Molecule type: DNA
A:Residues: 656-737 <LEAV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
R:Mutrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBU
A:Molecule type: DNA
A:Residues: 689-716, 'P', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g326720; PIDN:AA51991.1; PID:g235721
R:Kamino, K.; Ott, H.T.; Payami, H.; Wjisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
ataki, S.E.; Korenberg, J.R.; Shatman, V.; Kukull, W.; Larson, B.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415265
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AA523645.1; PID:g257378
A:Experimental source: Familial Alzheimer disease family 58
A:Note: sequence extracted from NCBI Backbone (NCBI:115374)
A:Accession: B44017
A:Molecule type: DNA

A:Residues: 687-718 <KAM2>
A:Cross-references: GB:545136; NID:g257379; PIDN:AA823646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A>Note: this sequence extracted from NCBI Backbone (NCBI:115376)
A>Note: this sequence has a silent mutation
R:Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfaced
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA6374.1; PID:g28526
A>Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A>Note: alternative splice form APP(751)
R:Goldgaber, D.; Lemman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <COL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ken
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muehlha
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DVR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g923612
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A>Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 267-367 <KIT>

A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g928611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M. P.; Rasool, C. G.; de Sauvage, F.; Vitek, S. M.; Bartus, R. T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 123-288, 'V', 365-770 <VT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VT3>
R:Zan, S. B.; Sallm, M.; Chou, W. G.; Sajdel-Sulkowska, E. M.; Majocha, R. E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M1874; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60
8 as Val, GUG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Maters, C.T.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K

Query Match	46.9%	Score 63;	DB 1;	Length 770;
Best Local Similarity	93.3%	Pred. No. 0.0015;		
Matches	14;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	DAEFRHDSGYEVHHK	15	
DB	672	DAEFRHDSGYEVHHQ	686	

RESULT 11
 JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 CSpecies: xenopus laevis (African clawed frog)
 CDate: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 CAccession: JH0773
 R.Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A.Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
 A.Reference number: JH0773; MUID:93129227; PMID:1282805
 A.Accession: JH0773
 A.Molecule type: mRNA
 A.Residues: 1-747 <OK>
 A.Cross-references: GB:SS2417; NID:g263150; PID:AA024653.1; PID:g263151
 A.Experimental source: larva
 C.Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C.Keywords: alternative splicing; amyloid
 F/287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

	Query Match	Score	DB	Length
Best Local Similarity	66.7%	Pred.	No. 0.19	
Matches	10; Conservative	4;	Mismatches	1; Indels
Gaps	0;			
Qy	1 DAEPRHDSGYEVHAK	15		
Db	649 DSEYRHDPTAYEVHHQ	663		

RESULT 12
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C/Accession: S23094
 R/Kojima, S.; Omori, M.
 PDBS Lett. 304, 57-60, 1992
 A>Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A/Reference number: S23094; MUID:92316198; PMID:1618299
 A/Accession: S23094
 A/Molecule type: protein
 A/Residues: 1-33 <K0>
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 36.2%; Score 64; DB 2; Length 33;
 Best Local Similarity 73.3%; Pred. No. 0.022;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKK 15
 |||||
 Db 6 DAEFRHDSGYEVHKK 20

RESULT 13
 VGNZRL
 cell fusion glycoprotein precursor - rinderpest virus (strain L)
 N/Contans: fusion glycoprotein F1; fusion glycoprotein F2
 C/Species: rinderpest virus
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
 C/Accession: A28921
 R/Tsukiyama, K.; Yoshikawa, Y.; Yamamuchi, K.
 Virology 164, 523-530, 1988
 A>Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
 A/Reference number: A28921; MUID:88219541; PMID:3285575
 A/Accession: A28921
 A/Molecule type: mRNA
 A/Residues: 1-546 <TSU>
 A/Cross-references: GB:M20870; NID:G333898; PIDN:AAA47399.1; PID:G333899
 C/Genetics:
 A/Genes: P
 C/Superfamily: parainfluenza virus cell fusion protein
 C/Keywords: glycoprotein; membrane fusion; transmembrane protein
 F/1-19/Domains: signal sequence #status predicted <SIG>
 F/20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
 F/105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
 F/109-133/Domains: transmembrane #status predicted <TM1>
 F/485-513/Domains: transmembrane #status predicted <TM2>
 F/25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.2%; Score 64; DB 1; Length 546;
 Best Local Similarity 61.1%; Pred. No. 0.49;
 Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 17 SITEIKGVYHRIETLIF 34
 |||||
 Db 283 SLSEIKGVYHRIETLSVSY 300

RESULT 14
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N/Alternate names: proteinase nexin II
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C/Accession: A27485; S19727; I59485
 R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A>Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
 A/Reference number: A27485; MUID:88106489; PMID:3322280
 A/Accession: A27485
 A/Molecule type: mRNA
 A/Residues: 1-695 <YAM>
 A/Cross-references: GB:M18373; NID:G191568; PIDN:AAA37139.1; PID:G309085
 A/Experimental source: brain
 R/de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991

A>Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A/Reference number: S19727; MUID:92096458; PMID:1756177
 A/Accession: S19727
 A/Molecule type: mRNA
 A/Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A/Cross-references: EMBL:X59379
 R/Iizumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
 Gene 112, 189-195, 1992
 A>Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A/Reference number: I49485; MUID:92209998; PMID:1555768
 A/Accession: I49485
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-19 <RBS>
 A/Cross-references: GB:D10603; NID:G220328; PIDN:BA01456.1; PID:G220329
 C/Genetics:
 A/Map position: 16C3
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C/Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 36.2%; Score 64; DB 2; Length 695;
 Best Local Similarity 73.3%; Pred. No. 0.64;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKK 15
 |||||
 Db 597 DAEFRHDSGYEVHKK 611

RESULT 15
 S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N/Alternate names: beta-A4 amyloid protein
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C/Accession: S00550; A41245; A39820; S46251
 R/Shivers, B.D.; Hlilich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A>Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A/Reference number: S00550; MUID:88312583; PMID:2900758
 A/Accession: S00550
 A/Molecule type: mRNA
 A/Residues: 1-695 <SHI>
 A/Cross-references: EMBL:X07648; NID:G55616; PIDN:CAA30488.1; PID:G55617
 R/Schubert, D.; Schroeder, R.; Lacobiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A>Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
 A/Reference number: A41245; MUID:88264430; PMID:2968652
 A/Accession: A41245
 A/Molecule type: protein
 A/Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A/Note: evidence for heparan sulfate attachment
 R/Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 PDBS Lett. 349, 109-116, 1994
 A>Title: The beta-A4 amyloid precursor protein binding to copper.
 A/Reference number: S46251; MUID:94320627; PMID:7913895
 A/Contents: annotation; copper binding sites
 A/Note: rat peptides were isolated but not sequenced
 R/Polompka, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A>Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
 A/Reference number: A39820; MUID:91217087; PMID:1673681
 A/Accession: A39820
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 18-32 <POT>
 A/Experimental source: brain
 C/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is c
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F/625-648/Domains: transmembrane #status predicted <TM>

Query Match 36.2%; Score 64; DB 2; Length 695;

Best Local Similarity 73.3%; Pred. No. 0.64;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DAERHDSGYVHRK 15
||| ||| ||| |||
Db 597 DAERHDSGYVHRK 611

Search completed: June 18, 2004, 20:03:31
Job time : 11.2209 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 6.67485 Seconds
(without alignments)

265.232 Million cell updates/sec

Title: US-09-865-294A-73

Perfect score: 177
Sequence: 1 DA6FRHDSGVVHAKISITIKGVIVRIETILE 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	46.9	57	A4_URSWA	Q29149 ursus fam1c
2	83	46.9	58	A4_CANFA	Q28280 canis fam1
3	83	46.9	58	A4_RABIT	Q28748 oryctolagus
4	83	46.9	58	A4_SHEEP	Q28757 ovis aries
5	83	46.9	59	A4_BOVIN	Q28053 bos taurus
6	83	46.9	751	A4_SAISC	Q95241 s amyloid b
7	83	46.9	770	A4_CAVPO	Q60495 c amyloid b
8	83	46.9	770	A4_HUMAN	P05067 h amyloid b
9	83	46.9	770	A4_MACFA	P53601 m amyloid b
10	83	46.9	770	A4_PIG	P79307 s amyloid b
11	64	36.2	546	A4_RINDL	P10864 rinderpest
12	64	36.2	770	A4_MOUSE	P12023 m amyloid b
13	64	36.2	770	A4_RAT	P08592 r amyloid b
14	61	34.5	546	A4_RAT	P41360 rinderpest
15	60	33.9	546	A4_RAT	P41356 rinderpest
16	59	33.3	546	A4_RAT	P41356 rinderpest
17	58	32.8	534	A4_RAT	P25032 measles vir
18	58	32.8	550	A4_RAT	P35973 measles vir
19	58	32.8	550	A4_RAT	P08300 measles vir
20	58	32.8	631	A4_RAT	P28886 phocine dis
21	57.5	32.5	356	A4_RAT	Q91695 arabisopsis
22	54	30.5	546	A4_RAT	P12574 rinderpest
23	52	29.4	220	A4_RAT	O48850 arabisopsis
24	52	29.4	229	A4_RAT	Q9na65 arabisopsis
25	51.5	29.1	539	A4_RAT	O14283 schistosach
26	51	28.8	207	A4_RAT	P53806 caenorhabdi
27	51	28.8	240	A4_RAT	Q9a376 arabisopsis
28	50.5	28.5	427	A4_RAT	P36049 saccharomyc
29	50	28.2	529	A4_RAT	P20031 measles vir
30	49.5	28.0	208	A4_RAT	O6p220 metahomoc
31	49.5	28.0	367	A4_RAT	Q91698 arabisopsis
32	49.5	28.0	4563	A4_RAT	P04114 homo sapien
33	49	27.7	231	A4_RAT	P07833 plasmodium

34	49	27.7	347	1	60MT COEUA	Q91e16 coptic japo
35	49	27.7	726	1	TRF BLADI	Q02942 blaberu di
36	49	27.7	925	1	P070T HUMAN	P57737 homo sapien
37	48.5	27.4	284	1	POLG PVYCH	P11897 potaco viru
38	48.5	27.4	327	1	POLG PVYCH	P21294 potaco viru
39	48	27.1	219	1	V721 ARATH	Q9ztw3 arabisopsis
40	48	27.1	221	1	V721 ARATH	P47192 arabisopsis
41	48	27.1	231	1	HGXR PLARG	P20035 plasmodium
42	48	27.1	449	1	TIG BALSO	Q8xyt8 raietonia s
43	48	27.1	810	1	CLPC BASCU	P37571 bacillus su
44	48	27.1	848	1	CLPC MYCTE	P24428 mycobacteri
45	48	27.1	848	1	CLPC MYCTU	O06286 mycobacteri

ALIGNMENTS

RESULT 1	A4_URSWA	STANDARD;	PRT;	57 AA.
AC	Q29149:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid			
DE	protein (Beta-Ap) (A-beta)] (Fragment).			
CN	APP.			
OS	Ursus maritimus (Polar bear) (Thalartoe maritimus).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.			
OX	NCBI_TaxID=29073;			
RN	[1]			
RP	SOURCE FROM N.A.			
RC	TISSUE=Brain;			
RE	MEDLINE=92017079; PubMed=1656157;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid			
RT	peptide in dog, polar bear and five other mammals by cross-species			
RT	polymerase chain reaction analysis."			
RL	Brain Res. Mol. Brain Res. 10:299-305 (1991).			
CC	-!- FUNCTION: Functional neuronal receptor which couples to			
CC	intracellular signaling pathway through the GTP-binding protein			
CC	G(O) (by similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Belongs to the APP family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
DR	EMBL; X56128; CAA39593.1; -.			
DR	PIR; B60045; B60045.			
DR	HSSP; P05067; 1BA4.			
DR	InterPro; IPR008155; A4_APP.			
DR	InterPro; IPR001355; Beta-APP.			
DR	Pfam; PF03494; Beta-APP; 1.			
DR	PROSITE; PS00319; A4-EXTRA; PARTIAL.			
DR	PROSITE; PS00320; A4-INTRA; PARTIAL.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.			
FT	NON TER	1		
FT	CHAIN	6	48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	<1	33	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	34	57	POTENTIAL.
FT	NON TER	57		
SQ	SEQUENCE	57 AA; 6172 MW;	8420988BA82DFA CRC64;	

Query Match: 46.9%; Score 83; DB 1; Length 57;
Best Local Similarity 93.3%; Pred. No. 3.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHMK 15
 DB 6 DAEFRHDSGYEVHMQ 20

RESULT 2

A4_CANFA STANDARD: PRT; 58 AA.
 ID_A4_CANFA
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (beta-Ap) (A-beta)] (fragment).
 GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Flesipedata; Canidae; Canis.
 NCBI_TaxId=9615;
 RX NCBI_TaxId=9615;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1 FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 SIMILARITY: Belongs to the APP family.
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 CC EMBL; X56125; CAA39590.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49
 FT DOMAIN <1 34
 FT TRANSMEM 35 58
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MM; 8469D488A2B12DFA CRC64;
 Query Match 46.9%; Score 83; DB 1; Length 58;
 Best Local Similarity 93.3%; Pred. No. 3.8e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHMK 15
 DB 7 DAEFRHDSGYEVHMQ 21

RESULT 3

A4_RABIT STANDARD: PRT; 58 AA.
 ID_A4_RABIT
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (beta-Ap) (A-beta)] (fragment).
 GN APP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxId=9986;
 RX NCBI_TaxId=9986;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1 FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 SIMILARITY: Belongs to the APP family.

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 CC EMBL; X56129; CAA39594.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48
 FT DOMAIN <1 33
 FT TRANSMEM 34 57
 FT DOMAIN 58 58
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MM; F434209D8BBA82D CRC64;

Query Match 46.9%; Score 83; DB 1; Length 58;
 Best Local Similarity 93.3%; Pred. No. 3.8e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHMK 15
 DB 6 DAEFRHDSGYEVHMQ 20

RESULT 4

A4_SHEEP STANDARD: PRT; 58 AA.
 ID_A4_SHEEP
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (beta-Ap) (A-beta)] (fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
 NCBI_TaxId=9940;
 RX NCBI_TaxId=9940;
 RN SEQUENCE FROM N.A.

```

CC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone B.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -i- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC -i- SIMILARITY: Belongs to the APP family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X56130; CA39595.1; -.
CC HSSP: P05067; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF03494; Beta-APP; 1.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1
CC CHAIN 1 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; P434209D88BBA82D CRC64;

Query Match 46.9%; Score 83; DB 1; Length 58;
Best Local Similarity 93.3%; Pred. No. 3; Be-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHRR 15
Db 6 DAEFRHDSGYEVHRR 20

RESULT 5
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC 028053;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DB protein (Beta-APP) (A-beta)] (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone B.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -i- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).

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CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC -i- SIMILARITY: Belongs to the APP family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.emb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X56124; CA39589.1; -.
CC HSSP: P05067; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF03494; Beta-APP; 1.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1
CC CHAIN 1 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 58 POTENTIAL.
CC DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
CC NON_TER 59 59
CC SEQUENCE 59 AA; 6414 MW; P43469D488A2E12D CRC64;

Query Match 46.9%; Score 83; DB 1; Length 59;
Best Local Similarity 93.3%; Pred. No. 3; Be-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHRR 15
Db 7 DAEFRHDSGYEVHRR 21

RESULT 6
A4_SAIISC STANDARD; PRT; 751 AA.
ID A4_SAIISC
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DB protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DB APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DB Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DB CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DB (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DB secretase C-terminal fragment 50); C31].
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy B., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -i- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tipe0 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).

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Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin I (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metalated APP induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPI domain possess protease inhibitor activity (By similarity).

FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including AFB family members, the APPA family, MAPK1p1, and SHC1. Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, APPB2, APPB1, IBI, KNS2 (via its TPR domain) (By similarity), APPB1 (via BASS) and DBP1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;

Name=APP770;

Isoid=Q95241-1; Sequence=Displayed;
Name=APP695;

Isoid=Q95241-2; Sequence=Not described;

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, s-APP-alpha and s-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at App-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

PTM: N-and O-glycosylated (By similarity).

CC	-1-PTM Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).
CC	-1-MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).
CC	Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).
CC	-1-SIMILARITY: Belongs to the APP family.
CC	-1-SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC	-----
DR	EMBL; S81024; AAD14347.1; ..
DR	HSSP; P05067; IAAI.
DR	InterPro; IPRO08155; A4_APP.
DR	InterPro; IPRO08154; A4_extra.
DR	InterPro; IPRO01255; Beta-APP.
DR	InterPro; IPRO02223; Kunitz_BPT1.
DR	Pfam; PF02177; A4_EXTRA; 1.
DR	Pfam; PF03494; Beta-APP; 1.
DR	Pfam; PF00014; Kunitz_BPT1; 1.
DR	PRINTS; PR00203; AMYLOIDA4.
DR	PRINTS; PR00759; BASICPTASR.
DR	ProDom; PD000222; Kunitz_BPT1; 1.
DR	SMART; SM00006; A4_EXTRA; 1.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00319; A4_EXTRA; 1.
DR	PROSITE; PS00320; A4_INTRA; 1.
DR	PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR	PROSITE; PS00279; BPT1_KUNITZ_2; 1.
KW	Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW	Coated pits; Neurons; Heparin-binding; Metal-binding; Copper; Iron;
KW	Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW	Proteoglycan; Amyloid; Alternative splicing.
FT	SIGNAL 1..17
FT	CHAIN 18..751
FT	CHAIN 18..668 SOLUBLE APP-ALPHA (POTENTIAL).
FT	CHAIN 18..652 SOLUBLE APP-BETA (POTENTIAL).
FT	CHAIN 653..751 C99 (POTENTIAL).
FT	CHAIN 653..694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT	CHAIN 653..692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT	CHAIN 669..751 C83 (POTENTIAL).
FT	CHAIN 669..694 P3(42) (POTENTIAL).
FT	CHAIN 669..692 P3(40) (POTENTIAL).
FT	CHAIN 693..751 GAMMA-CTF(59) (POTENTIAL).
FT	CHAIN 693..751 GAMMA-CTF(57) (POTENTIAL).
FT	CHAIN 702..751 GAMMA-CTF(50) (POTENTIAL).
FT	CHAIN 721..751 C31 (POTENTIAL).
FT	CHAIN 721..751 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 18..680 POTENTIAL.
FT	TRANSMEM 681..704 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 705..751 HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN 96..110 ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN 181..188 BPT1/KUNITZ INHIBITOR.
FT	DOMAIN 291..341 HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN 316..344 HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN 363..428 COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN 504..521 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT	DOMAIN 713..732 ASP/GLU-RICH (ACIDIC).
FT	DOMAIN 230..260 POLY-TNR.
FT	DOMAIN 274..280 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT	SITE 144..144 REACTIVE BOND.
FT	ACT_SITE 301..302 CLEAVAGE (BY BETA-SECRETASE)
FT	SITE 652..653

FT SITE 653 654 (BY SIMILARITY).
 FT SITE 666 669 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 685 685 (BY SIMILARITY).
 FT SITE 687 687 INVOLVED IN FREE RADICAL PROPAGATION
 FT SITE 687 687 (BY SIMILARITY).
 FT SITE 692 693 INVOLVED IN OXIDATIVE REACTIONS
 FT SITE 692 693 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 FT SITE 694 695 (BY SIMILARITY).
 FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 FT SITE 705 715 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 FT SITE 720 721 (BY SIMILARITY).
 FT SITE 738 741 BASOLATERAL SORTING SIGNAL
 FT SITE 740 743 (BY SIMILARITY).
 FT SITE 743 743 CLEAVAGE (BY CASPASES-3, -6, -8 OR -9)
 FT SITE 743 743 (BY SIMILARITY).
 FT SITE 743 743 ENDOCYTOSIS SIGNAL.
 FT SITE 743 743 NPXY MOTIF.
 Query Match 46.9%; Score 83; DB 1; Length 751;
 Best Local Similarity 93.3%; Pred. No. 0.00058;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKK 15
 Db 653 DAEFRHDSGYEVHKK 667

RESULT 7
 A4 CAVPO STANDARD; PRT: 770 AA.
 ID 060495; 060496; 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP
 OS Cavia porcellus (Guinea pig).
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver; PubMed=9116031;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mackic J.B., Mateubara E., Govereale S., Miguel C.,
 RA Mao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein.";

RL Neuroscience 95:243-254(2000).
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007;
 RA Plimix I., Matsuura U., Yun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma-secretase assay based on detection of the putative
 RT C-terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tipe6 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G(0) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPKIP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPB1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via Bass) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of APP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipitated,
 CC APOE3 appears to be the preferred amyloid binding isoform, while
 CC the APOE4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=060495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=060495-2; Sequence=VSP_007221, VSP_007222;
 CC TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are

predominantly expressed in peripheral organs such as muscle and liver.

-1- INDUCTION: Increased levels during neuronal differentiation.

-1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue (by similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/ntcsestrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTFb).

-1- PTM: Proteolytically cleaved by caspase-3 during neuronal apoptosis (by similarity).

-1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to the L-APP isoforms produces the APP proteoglycan core proteins, the apicaps (by similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific (by similarity).

Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins.

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (by similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates.

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.

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EMBL: X97631; CAA66230.1; -
EMBL: X99198; CAA67589.1; -
HSSP: P05067; 1BA4
InterPro: IPR008155; A4_APP
InterPro: IPR008154; A4_extra
InterPro: IPR002223; Kunitz_BPT1
Pfam: PF000014; Kunitz_BPT1; 1.
PRINTS: PR00203; AMYLOIDA4
PRINTS: PR00759; BASICPTASE
ProDom: PD000222; Kunitz_BPT1; 1.
SMART: SM00131; KU; 1.
PROSITE: PS00319; A4_EXTRA; 1.
PROSITE: PS00320; A4_INTRA; 1.
PROSITE: PS00280; BPT_KUNITZ_1; 1.
PROSITE: PS00279; BPT_KUNITZ_2; 1.
ApocToxas: Endocytosis; Cell adhesion; Serine protease inhibitor;
Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;

KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1
FT CHAIN 1 17
FT CHAIN 1 8 770
FT CHAIN 1 8 687
FT CHAIN 1 8 671
FT CHAIN 1 8 770
FT CHAIN 672 713
FT CHAIN 672 713
FT CHAIN 672 713
FT CHAIN 688 770
FT CHAIN 688 713
FT CHAIN 688 711
FT CHAIN 712 770
FT CHAIN 714 770

Query Match
Best local Similarity 93.3%; Score 83; DB 1; Length 770;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRDSDGVEYHKK 15
672 DAEFRDSDGVEYHQQ 686

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
ID A4_HUMAN P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BT38; Q9UC49; Q9UCB6; Q9UC8A; Q9UCD1; Q9UC58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)); Gamma-CRF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)); Gamma-CRF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)); C31].
DE APP OR A4 OR AD1.
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Graesche K.-H., Multhaup G., Beyreuther K., Mueller-Hill B., "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
RT Nature 325:733-736(1987).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Pontee P., Gonzalez-Dewailly F., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.,
RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors.";
RT Nature 331:525-527(1998).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2763775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.,
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522 (1989).

[14]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RX MEDLINE=92268136; PubMed=1587857;
RC TISSUE=Leukocyte;
RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RA Tang K., Mang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
RA Brownstein M.J., Ueda T.B., Toshimuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttenfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sedlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sedlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).

[12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Pauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.B., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=8122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lampert B.D., Villa-Komaroff L.,
RA Guejila J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Tanahashi Y., Tokuhima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Behar D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717, AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Demian R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;

RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.: Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [22]

Query Match 46.9%; Score 83; DB 1; Length 770;
 Best Local Similarity 93.3%; Pred. No. 0.0006; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHMK 15
 |||||
 Db 672 DAEFRHDSGYEVHMQ 686

RESULT 9
 A4_MACFA STANDARD; PRT; 770 AA.
 AC P53601: 095K07;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31).
 GN APP.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cetartiodactyla;
 OC Cercopithecoidea; Macaca.
 ON NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podilany M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease.";
 RL Am. J. Pathol. 138:1423-1435 (1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPK3IP1, and SHC1, Numb and Dab1 (By similarity). Binding

CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPB2, IBI, KNS2
 CC (via its TPR domains) (By similarity). APPB2 (via BASS) and DBP1.
 CC In vitro, it binds MAPK via the NP-binding domain (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@ebi.ac.uk).

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CC -----
DR EMBL; M58727; AAA36829.1; -
DR EMBL; M58726; AAA36828.1; -
DR HSSP; P05067; AAP.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
PT SIGNAL 1 17
PT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
PT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
PT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
PT CHAIN 672 770 C99 (POTENTIAL).
PT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
PT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
PT CHAIN 688 770 C83 (POTENTIAL).
PT CHAIN 688 713 P3(42) (POTENTIAL).
PT CHAIN 688 711 P3(40) (POTENTIAL).
PT CHAIN 712 770 GANMA-CTF(59) (POTENTIAL).
PT CHAIN 714 770 GANMA-CTF(57) (POTENTIAL).
PT CHAIN 721 770 GANMA-CTF(50) (POTENTIAL).
PT CHAIN 740 770 C31 (POTENTIAL).
PT CHAIN 18 699 EXTRACELLULAR (POTENTIAL).
PT TRANSMEM 700 723 POTENTIAL.
PT DOMAIN 724 770 CYTOSOLSMIC (POTENTIAL).
PT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
PT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
PT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
PT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
PT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
PT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
PT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
PT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
PT DOMAIN 274 280 POLY-THR.
PT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
PT ACT SITE 301 302 REACTIVE BOND (BY SIMILARITY).
PT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
PT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
PT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
PT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
PT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
PT SITE 711 712 CLEAVAGE (BY GANMA-SECRETASE; SITE 1) (BY SIMILARITY).
PT SITE 713 714 CLEAVAGE (BY GANMA-SECRETASE; SITE 2) (BY SIMILARITY).
PT SITE 720 721 CLEAVAGE (BY GANMA-SECRETASE; SITE 3) (BY SIMILARITY).
PT SITE 724 734 BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
PT SITE 739 740 CLEAVAGE (BY CASPASES-3, -6, -8 OR -9)

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Query Match 46.9%; Score 83; DB 1; Length 770;
Best Local Similarity 93.3%; Pred. No. 0.006;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPHDSGYEVHNR 15
DB 672 DAEPHDSGYEVHNR 686

RESULT 10
ID A4_PIG STANDARD; PRT; 770 AA.
AC P79307; Q29023; Q9T010;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
DS Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE OF 1-136 FROM N.A.
RC TISSUE=Small intestine;
RA Winterer A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE OF 667-723 FROM N.A.
RC TISSUE=Brain;
RA MEDLIN=92017079; Pubmed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tipe0 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

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cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1. Mumb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, PPR1, APBP1, H1, KNS2 (via its 7PR domain) (By similarity), APBP2 (via Bass) and DDB1. In vitro, it binds MAP7 via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-1- DOMAIN: The NPYX sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPYX motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPYX site is also involved in clathrin-mediated endocytosis (By similarity).

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/alpha-secretase-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-1- PTM: N- and O-glycosylated (By similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).

-1- Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 EMBL, AB032550; BAA84580.1; -

DR	EMBL; Z84022; CAB06313.1; -	FT	1	17	BY SIMILARITY.
DR	EMBL; X56127; CAA39592.1; -	FT	18	770	AMYLOID BETA A4 PROTEIN.
DR	HSSP; P05067; LAAP.	FT	18	687	SOLUBLE APP-ALPHA (POTENTIAL).
DR	InterPro: IPR008155; A4_APP.	FT	18	671	SOLUBLE APP-BETA (POTENTIAL).
DR	InterPro: IPR008155; A4_APP.	FT	672	770	C99 (BY SIMILARITY).
DR	InterPro: IPR002223; Kunitz_BPTI.	FT	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
DR	Pfam; PF02177; A4_EXTRA; 1.	FT	672	711	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
DR	PRINTS; PR00203; AMYLOIDA4.	FT	688	770	C83 (BY SIMILARITY).
DR	PRINTS; PR00759; BASICPTASE.	FT	688	713	P3(42) (BY SIMILARITY).
DR	PRODOM; PD000222; Kunitz_BPTI; 1.	FT	688	711	P3(40) (BY SIMILARITY).
DR	SMART; SM00006; A4_EXTRA; 1.	FT	712	770	GAMMA-CTF(59).
DR	SMART; SM00131; KU; 1.	FT	714	770	GAMMA-CTF(57).
DR	PROSITE; PS00319; A4_EXTRA; 1.	FT	721	770	GAMMA-CTF(50) (BY SIMILARITY).
DR	PROSITE; PS00320; A4_INTRA; 1.	FT	740	770	C31 (DURING APOPTOSIS) (BY SIMILARITY).
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.	FT	18	699	EXTRACELLULAR (POTENTIAL).
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.	FT	700	723	POTENTIAL.
KW	Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neutrophil; Heparin-binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation; Amyloid.	FT	724	770	CYTOSOLIC (POTENTIAL).
KM		FT	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	FT	135	155	COOPER-BINDING (BY SIMILARITY).
FT	CHAIN	FT	181	188	ZINC-BINDING (BY SIMILARITY).
FT	CHAIN	FT	291	341	BPTI/KUNITZ INHIBITOR.
FT	CHAIN	FT	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	FT	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	CHAIN	FT	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	CHAIN	FT	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT	DOMAIN	FT	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	FT	274	280	POLY-THR.
FT	DOMAIN	FT	144	144	REQUIRED FOR COPPER (II) REDUCTION (BY SIMILARITY).
FT	SITE	FT	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	FT	671	672	CLEAVAGE (BY BETA-SECRETASE3) (BY SIMILARITY).
FT	ACT SITE	FT	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	FT	687	688	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT	SITE	FT	704	704	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT	SITE	FT	706	706	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT	SITE	FT	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT	SITE	FT	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT	SITE	FT	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT	SITE	FT			
Query Match	1	DAEFRHDSGYEVHHK	15	46.9%	Score 83; DB 1; Length 770;
Best Local Similarity	14	DAEFRHDSGYEVHHK	15	53.3%	Pred. No. 0.0006;
Matches	14	DAEFRHDSGYEVHHK	15	53.3%	Indels 0; Gaps 0;
DB	672	DAEFRHDSGYEVHHK	686		

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RESULT 11
VGLF_RINDL STANDARD; PRT; 546 AA.
AC P10864;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain L) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirinae.
OX NCBI_TaxID=11243;
RN
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219541; PubMed=3285575;
RA Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
sequence of the F mRNA, and several features of the F protein.";
RL Virology 164:523-530(1988).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20870; AAA47399.1; -.
DR F1; A28921; VGNZRL.
DR HSSP; P04849; ISVF.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; Fusion_gly.1.
KM Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT STGNL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58911 MW; 985029418F28F85 CEC64;
Query Match 36.2%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.21;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 17 SITEKGVVHRTITL 34
Db 283 SLSEIKGVVHRTLSVS 300

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homology) (amyloidogenic glycoprotein) (AG) [contains:
DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CRF(59) (Gamma-secretase
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-CRF(57) (Gamma-secretase C-terminal fragment 57)
DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CRF(50)
DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE 50) (AID(50)); C31].
GN App.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
[1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Puruya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN
[2]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN
[3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., Van Leuven F., Van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN
[4]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX STRAIN=SAMP8; TISSUE=Hippocampus;
RX MEDLINE=21130647; PubMed=11235921;
RA Kumar V.B., Vyae K., Franko M., Choudhary V., Buddhireja C.,
RA Alvarez J., Morley J.B.;
RT "Molecular cloning, expression, and regulation of hippocampal amyloid
RT precursor protein of senescence accelerated mouse (SAMP8).";
RL Biochem. Cell Biol. 79:57-67(2001).
RN
[5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikaki S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN
[6]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RX TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Blat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,

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RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [17]
 RN SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [18]
 RN SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Msd domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [19]
 RN SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblatt K., Capecci M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RN TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Menged G., Ghetti B., Palacios J.M., Triathou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RN INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-1.";
 RL Neuron 28:449-459(2000).
 RN [12]
 RN C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Mikura T., Hiraki T.,
 RA Kiyakia J.M., Nishimoto I.,
 RA "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RN INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=21202801; PubMed=11912189;
 RA Tatu H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RN INTERACTION OF CTF PEPTIDES WITH NOMB.
 RX MEDLINE=22008109; PubMed=12011466;
 RA Roncarati R., Sestran N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Menucci O., McGlade J.C., Rakic P., D'Adamo L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid
 RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]

RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APPB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cuypers P., Orlans I., Cressaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RT nuclear fraction of neurons in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APPB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G10 and JIP. Inhibits G10 alpha APPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, FPR1, APPBP1, IBI, KNS2 (via its TPR domains), APPB2 (via
 CC Bass) and Ddb1 (By similarity). In vitro, it binds MAPK via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CERN17 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 36.2%; Score 64; DB 1; Length 770;
 Best Local Similarity 73.3%; Pred. No. 0.3;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DAEPHDSGVYVHRK 15
 DB 672 DAEPHDSGVYVHRQ 686

RESULT 13
 A4 RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-ARG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble
 DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
 DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
 DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
 DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);

DE Gamma-Ctf(50) (Gamma-secretase C-terminal fragment 50); C311.
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=83112583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RT Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1165-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=69183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=11483588;
RA Gu Y., Missonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandorink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95263526; PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopolou D.,
RT Mylliceu C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=97150061; PubMed=8996834;
RA Sandorink R., Manning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DBP1, AND MUTAGENESIS OF TYR-757, ASN-759 AND
RP TYR-762.
RX MEDLINE=99127916; PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RT Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DBP) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX MEDLINE=99162676; PubMed=10024358;
RA Brouillet E., Tremblay A., Galianud D., Volovitch M., Bouillat C.,
RT Valenza C., Prochiantz A., Alliquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10368-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.B.,
RA Scarpa R.C., Cuaungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.B.,
RT Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460;
RA Kanaki J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochem. Biophys. Res. Commun. 158:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;
RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.B.,
RA Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [14]
RP PHOSPHORYLATION ON SER-730.
RX MEDLINE=99262094; PubMed=10329382;
RA Isohara T., Horitachi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA Greengard P., Nairn A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [15]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [16]
RP PHOSPHORYLATION ON THR-743.
RX MEDLINE=20396183; PubMed=10936190;
RA Iijima K.-I., Ando K., Takeda S., Sacho Y., Seki T., Itohara S.,
RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT protein by cyclin-dependent kinase 5.";
RL J. Neurochem. 75:1085-1091(2000).
RN [17]
RP CARBOHYDRATE STRUCTURE OF APPICAN.
RX MEDLINE=21463085; PubMed=11479316;
RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.;
RT "Appican, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate B in the repeating disaccharide region
RT and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
RN [18]
RP FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to

CC -----
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DR EMBL; Z30700; CAA83186.1; -;
DR EMBL; Z30697; CAA83181.1; -;
DR PIR; S47305; S47305.
DR HSSP; P04849; ISVP.

DR Interpro: IPR000776; Fusion gly.
DR Pfam: PF00523; fusion_gly; 1.

KM Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.

FT SIGNAL	1	19	
FT CHAIN	20	546	FUSION GLYCOPROTEIN P0.
FT CHAIN	20	108	P2 PROTEIN.
FT CHAIN	109	546	P1 PROTEIN.
FT DOMAIN	104	108	ARG/LYS-RICH (BASIC).
FT TRANSMEM	109	133	POTENTIAL.
FT TRANSMEM	484	513	POTENTIAL.
FT DOMAIN	514	517	ARG/LYS-RICH (BASIC).
FT DISULFID	64	191	LINKAGE BETWEEN P2 & P1 (POTENTIAL).
FT CARBOHYD	25	25	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	57	57	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	63	63	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	518	518	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE	546 AA;	58705 MW;	ED3DP8AFPDBCB95 CRC64;

Query Match 33.9%; Score 60; DB 1; Length 546;
Best local Similarity 55.6%; Pred. No. 0.77;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 17 SITEIKGVIVRIETILF 34
|:|||||:|:|:|:|:
Db 283 SLSEIKGVIVRIETILF 300

Search completed: June 18, 2004, 19:59:38
Job time : 7.67485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 32.9571 Seconds

(without alignment)
325.503 Million cell updates/sec

Title: US-09-865-294A-73

Perfect score: 177

Sequence: 1 DAEFRHDSGYEVHHKISTEIKGVIVARIETILP 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	85	48.0	82	4 Q16014	Q16014 homo sapien
2	83	46.9	19	4 Q9UC8	Q9UC8 homo sapien
3	83	46.9	28	4 Q9UCD1	Q9UCD1 homo sapien
4	83	46.9	30	4 Q9UC9A	Q9UC9A homo sapien
5	83	46.9	32	4 Q9UCJ3	Q9UCJ3 homo sapien
6	83	46.9	82	4 Q16020	Q16020 homo sapien
7	83	46.9	82	4 Q16019	Q16019 homo sapien
8	83	46.9	113	13 Q8JH58	Q8JH58 chelydra se
9	83	46.9	534	13 Q9J296	Q9J296 gallus gall
10	83	46.9	569	13 Q9PVL1	Q9PVL1 gallus gall
11	83	46.9	695	13 Q9PGL8	Q9PGL8 gallus gall
12	83	46.9	751	13 Q9DGL7	Q9DGL7 gallus gall
13	78	44.1	35	4 Q8WZ99	Q8WZ99 homo sapien
14	68	38.4	693	13 Q98SG0	Q98SG0 xenopus lae
15	68	38.4	695	13 Q98SFP9	Q98SFP9 xenopus lae
16	68	38.4	695	13 Q7ZXQ0	Q7ZXQ0 xenopus lae

17	68	38.4	747	13 Q91963	Q91963 xenopus. ap
18	64	36.2	79	11 Q35463	Q35463 cricetus
19	64	36.2	218	11 Q8BPC7	Q8BPC7 mus musculus
20	64	36.2	384	11 Q8BPC7	Q8BPC7 mus musculus
21	63	35.6	699	13 Q57394	Q57394 narke japon
22	61	34.5	546	12 Q91HA5	Q91HA5 rinderpest
23	60	33.9	546	12 Q84926	Q84926 peste-des-p
24	59	33.3	528	12 Q9YJW9	Q9YJW9 canine dist
25	59	33.3	530	12 Q8QV06	Q8QV06 canine dist
26	59	33.3	552	12 Q66147	Q66147 cetacean mo
27	59	33.3	662	12 Q9DX22	Q9DX22 canine dist
28	59	33.3	662	12 Q91KX3	Q91KX3 canine dist
29	59	33.3	662	12 Q9YKJ7	Q9YKJ7 canine dist
30	59	33.3	662	12 Q89327	Q89327 canine dist
31	58	32.8	319	10 Q91RT3	Q91RT3 arabidopsis
32	58	32.8	534	12 Q04243	Q04243 measles vir
33	58	32.8	537	12 Q04242	Q04242 measles vir
34	58	32.8	545	12 Q9PYX4	Q9PYX4 measles vir
35	58	32.8	550	12 P90331	P90331 measles vir
36	58	32.8	550	12 Q9QEX0	Q9QEX0 measles vir
37	58	32.8	550	12 Q9QEX9	Q9QEX9 measles vir
38	58	32.8	550	12 P90330	P90330 measles vir
39	58	32.8	550	12 Q9QEW7	Q9QEW7 measles vir
40	58	32.8	550	12 Q9QMK4	Q9QMK4 measles vir
41	58	32.8	550	12 Q89495	Q89495 measles vir
42	58	32.8	550	12 Q8V049	Q8V049 measles vir
43	58	32.8	550	12 Q9YJ94	Q9YJ94 measles vir
44	58	32.8	550	12 Q9QEX1	Q9QEX1 measles vir
45	58	32.8	550	12 Q9QEW8	Q9QEW8 measles vir

ALIGNMENTS

RESULT 1

ID	Q16014	PRELIMINARY:	PRT:	82 AA.
AC	Q16014:			
DT	01-NOV-1996 (TRENBLREL. 01, Created)			
DT	01-NOV-1996 (TRENBLREL. 01, Last sequence update)			
DT	01-JUN-2003 (TRENBLREL. 24, Last annotation update)			
DE	Beta-amyloid peptide (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9323601; PubMed=8476439;			
RA	Demman R.B., Rosenzweig R., Miller D.L.;			
RT	"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."			
RL	Biochem. Biophys. Res. Commun. 192:96-103(1993).			
DR	EMBL; S60721; AAB26263.2; -.			
DR	HSSP; P05067; 1BA4.			
DR	GO:0016020; C-membrane; IRA.			
DR	InterPro; IPR001255; Beta-APP.			
DR	Pfam; PF03494; Beta-APP; 1.			
FT	NON TER			
FT	NON TER			
SQ	SEQUENCE 82 AA; 8972 MW; P534A5B3EA9230A CRC64;			

Query Match 48.0%; Score 85; DB 4; Length 82;
Best Local Similarity 43.5%; Pred. No. 0.00013;
Matches 20; Conservative 5; Mismatches 9; Indels 12; Gaps 2;

QY 1 DAEFRHDSGYEVHHKISTEIKGVIVARIETILP 34
DB 18 DAEFRHDSGYEVHHKISTEIKGVIVARIETILP 34

RESULT 2

Q9UC8

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ID Q9UC8      PRELIMINARY; PRT; 19 AA.
AC Q9UC8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid (1-42) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=94068497; PubMed=8248178;
RA Rober A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA Gowing E., Ball M.J.;
RT "beta-amyloid (1-42) is a major component of cerebrovascular amyloid
RT deposits: implications for the pathology of Alzheimer disease.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR HSSP; P05067; IAMB.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 19 AA; 2315 MW; 05802B3F6DDCE3E CRC64;

Query Match 46.9%; Score 83; DB 4; Length 19;
Best Local Similarity 93.3%; Pred. No. 5.1e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 1 DAEFRHDSGYEVHHQ 15

RESULT 3
Q9UCD1 PRELIMINARY; PRT; 28 AA.
ID Q9UCD1;
AC Q9UCD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=94045685; PubMed=8229004;
RA Vigo-Pelfrey C., Lee D., Kelm P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RT J. Neurochem. 61:1965-1968(1993).
DR HSSP; P05067; IAMB.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 28 AA; 3244 MW; DB7BD081160AFC81 CRC64;

Query Match 46.9%; Score 83; DB 4; Length 28;
Best Local Similarity 93.3%; Pred. No. 7.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 1 DAEFRHDSGYEVHHQ 15

RESULT 4
Q9UC9 PRELIMINARY; PRT; 30 AA.
ID Q9UC9;
AC Q9UC9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy B., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RT Ann. Neurol. 35:245-246(1994).
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match 46.9%; Score 83; DB 4; Length 30;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 1 DAEFRHDSGYEVHHQ 15

RESULT 5
Q9UC3 PRELIMINARY; PRT; 33 AA.
ID Q9UC3;
AC Q9UC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RT Nature 359:325-327(1992).
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFB2F4167ABD0 CRC64;

Query Match 46.9%; Score 83; DB 4; Length 33;
Best Local Similarity 93.3%; Pred. No. 9.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
DB 1 DAEFRHDSGYEVHHQ 15

RESULT 6
Q16020 PRELIMINARY; PRT; 82 AA.
ID Q16020;
AC Q16020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AASB5D9230A CRC64;
Query Match 46.9%; Score 83; DB 4; Length 82;
Best Local Similarity 93.3%; Pred. No. 0.00025;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHK 15
DB 18 DAEFRHDSGYEVHHQ 32
RESULT 7
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AASB5D9230A CRC64;
Query Match 46.9%; Score 83; DB 4; Length 82;
Best Local Similarity 93.3%; Pred. No. 0.00025;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHK 15
DB 18 DAEFRHDSGYEVHHQ 32
RESULT 8
ID Q8JH58 PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)

DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OC NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RL protein family in the hypothalamus of the snapping turtle, Chelydra
RL serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -.
DR GO; GO:0016020; C:membrane; IRA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT NON_TER 12750
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
Query Match 46.9%; Score 83; DB 13; Length 113;
Best Local Similarity 93.3%; Pred. No. 0.00036;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHK 15
DB 15 DAEFRHDSGYEVHHQ 29
RESULT 9
ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Amyloid protein (Fragment).
GN Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.B.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IRA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT NON_TER 534
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2866D4C92 CRC64;
Query Match 46.9%; Score 83; DB 13; Length 534;
Best Local Similarity 93.3%; Pred. No. 0.00025;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHK 15
DB 15 DAEFRHDSGYEVHHQ 29

Db 436 DAEFRHDSGYEVHHQ 450

RESULT 10

Q9PVL1 PRELIMINARY; PRT; 569 AA.

AC Q9PVL1 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.,
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 46.9%; Score 83; DB 13; Length 569;
Best Local Similarity 93.3%; Pred. No. 0.0022;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
Db 472 DAEFRHDSGYEVHHQ 486

RESULT 11
Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX (1)
RN SEQUENCE FROM N.A.
RP Sarasa M., Rodolosse A., Sorribas V.,
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; B78B9413A8033D84 CRC64;

DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 46.9%; Score 83; DB 13; Length 695;

Best Local Similarity 93.3%; Pred. No. 0.0027;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15

Db 597 DAEFRHDSGYEVHHQ 611

RESULT 12

Q9DGJ7 PRELIMINARY; PRT; 751 AA.

AC Q9DGJ7 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX (1)
RN SEQUENCE FROM N.A.
RP Sarasa M., Rodolosse A., Sorribas V.,
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:004867; P:serine protease inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PR00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PRINTS; PR00759; BASICTYASB.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KJ; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; B78B9413A8033D84 CRC64;

Query Match 46.9%; Score 83; DB 13; Length 751;
Best Local Similarity 93.3%; Pred. No. 0.0029;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHK 15
Db 653 DAEFRHDSGYEVHHQ 667

RESULT 13
Q8WZ99 PRELIMINARY; PRT; 35 AA.
AC Q8WZ99 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

```

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maturani Y., Nimomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,
RA Wada-Isoe K., Yamagata K., Ohno K., Tsuduki S., Saito T.,
RA Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel missense mutation (D678N) of amyloid precursor protein gene in
RT a Japanese pedigree of familial Alzheimer's disease."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB06441; BAB71958.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 35 AA; 4084 MW; 49D7D17289743B71 CRC64;

Query Match 44.1%; Score 78; DB 4; Length 35;
Best Local Similarity 86.7%; Pred. No. 0.00053;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
Db 17 DAEFRHDSGYEVHHQ 31

RESULT 14
ID Q98SGO PRELIMINARY; PRT; 693 AA.
AC Q98SGO;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-amyloid precursor protein A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1H23.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4-extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAP1DF655C1AB653 CRC64;

Query Match 38.4%; Score 68; DB 13; Length 693;
Best Local Similarity 66.7%; Pred. No. 0.4;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
Db 595 DSEYRHDAEYEVHHQ 609

```

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RESULT 15
ID Q98SP9 PRELIMINARY; PRT; 695 AA.
AC Q98SP9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-amyloid precursor protein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298151; CAC37194.1; -.
DR HSSP; P05067; 1H23.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4-extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78803 MW; DC14EB02A1B0204A CRC64;

Query Match 38.4%; Score 68; DB 13; Length 695;
Best Local Similarity 66.7%; Pred. No. 0.41;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
Db 597 DSEYRHDAEYEVHHQ 611

```

Search completed: June 18, 2004, 20:02:29
 Job time : 32.9571 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 18, 2004, 19:49:20 ; Search time 69.2025 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-74

Perfect score: 247
Sequence: 1 DAERHDSGVENHVKLVF.....KISTIKGVVHRIETLF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	100.0	48	AAE35680	AAE35680 Human Abe
2	163	66.0	100	AAE14375	AAE14375 Human Abe
3	163	66.0	108	AAE14383	AAE14383 Gamma-sec
4	163	66.0	112	AAE35356	AAE35356 Familial
5	163	66.0	695	AAW19484	AAW19484 APP695 mu
6	163	66.0	695	AAW19498	AAW19498 APP695 mu
7	163	66.0	695	AAW88436	AAW88436 Human APP
8	163	66.0	695	AAU07207	AAU07207 Human bet
9	163	66.0	695	AAE10634	AAE10634 Human amy
10	163	66.0	695	AAE06864	AAE06864 Human amy
11	163	66.0	695	AAE02586	AAE02586 Human amy
12	163	66.0	695	AAU06608	AAU06608 Human Amy
13	163	66.0	695	ABB78595	ABB78595 Human APP
14	163	66.0	697	AAW88430	AAW88430 Human APP
15	163	66.0	697	AAU07210	AAU07210 Human bet
16	163	66.0	697	AAE10637	AAE10637 Human amy
17	163	66.0	697	AAE06867	AAE06867 Human amy
18	163	66.0	697	AAE02589	AAE02589 Human amy
19	163	66.0	697	AAU06611	AAU06611 Human Amy
20	163	66.0	697	ABB78598	ABB78598 Human APP
21	163	66.0	751	AAW19486	AAW19486 APP751 mu
22	163	66.0	751	AAW19499	AAW19499 APP751 mu
23	163	66.0	770	AAW19485	AAW19485 APP770 mu
24	163	66.0	770	AAW19500	AAW19500 APP770 mu
25	163	66.0	770	AAE06913	AAE06913 Human amy

26	161.5	65.4	42	2	AAE65288	AAE65288 Beta amy1
27	160	64.8	34	6	AAE35679	AAE35679 Human Abe
28	158.5	64.2	42	2	AAE65287	AAE65287 Beta amy1
29	158	64.0	118	2	AAE50030	AAE50030 APP C-ter
30	157	63.6	47	2	AAW81475	AAW81475 Synthetic
31	157	63.6	48	4	AAE37523	AAE37523 Amyloid p
32	157	63.6	52	2	AAE64166	AAE64166 Variant b
33	157	63.6	52	2	AAW81476	AAW81476 Synthetic
34	157	63.6	52	6	ABU08712	ABU08712 Amyloid b
35	157	63.6	52	6	ABP97924	ABP97924 Amino aci
36	157	63.6	52	6	ADA90299	ADA90299 Abeta aml
37	157	63.6	53	2	AAE55695	AAE55695 Sequence
38	157	63.6	53	6	ABU08708	ABU08708 Amyloid b
39	157	63.6	53	7	ADB61450	ADB61450 Amyloid b
40	157	63.6	54	3	AAE32126	AAE32126 Amyloid-b
41	157	63.6	55	4	AAE11482	AAE11482 Human APP
42	157	63.6	59	2	AAW05375	AAW05375 Amyloid p
43	157	63.6	59	2	AAW70863	AAW70863 Beta-amy1
44	157	63.6	59	4	AAE84425	AAE84425 Partial s
45	157	63.6	60	3	AAE69701	AAE69701 Beta-amy1

ALIGNMENTS

RESULT 1

ID AAE35680 standard; peptide; 48 AA.

XX AAE35680;

XX 23-OCT-2003 (revised)

DT 17-JUN-2003 (first entry)

XX Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.

XX Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;

XX Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;

XX vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.

XX Homo sapiens.

XX Measles virus.

XX Chimeric.

XX Key Location/Qualifiers

XX Region 1..28

XX Region /note= "Human beta amyloid peptide"

XX Region 32..48

XX Region /note= "Measles virus T helper cell epitope"

XX WO200296350-A2.

XX 05-DEC-2002.

XX 02-APR-2002; 2002WO-US010293.

XX 25-MAY-2001; 2001US-00865294.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CX;

XX WPI; 2003-201258/19.

XX Novel peptide immunogen comprising a helper T cell epitope, an N-terminal

PT fragment of amyloid beta peptide linked to the epitope, and optionally a

PT spacer, useful for preventing or treating Alzheimer's disease.

XX Claim 9; Page 39; 77pp; English.

XX The present invention relates to a novel peptide immunogen comprising a

CC helper T cell (TH) epitope, an N-terminal fragment of amyloid beta

CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

CC Sequence 48 AA;

Query Match 100.0%; Score 247; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 5e-27; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFPADGVGSKKISITIRIKGVIVRIETILF 48
DB 1 DAEFRHDSGYEVHHQKLVFPADGVGSKKISITIRIKGVIVRIETILF 48

RESULT 2
AAE14375
ID AAE14375 standard; peptide; 100 AA.

AAE14375;

12-MAR-2002 (first entry)

Amyloid precursor protein beta-CTF domain #5.

Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
APP; beta-secretase; Alzheimer's disease.

Unidentified.

MO200183811-A1.

08-NOV-2001.

25-APR-2001; 2001WO-US013332.

01-MAY-2000; 2000US-0201053P.

(MERI) MERCK & CO INC.

Li Y, Xu M, Huang Q, Gardell S;

WPI; 2002-066536/09.

Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.

Claim 3; Page 6; 36pp; English.

The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the

CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's
CC disease, and in the characterisation of the biological importance of
CC gamma-secretase. The present sequence is a beta-CTF domain used in the
CC invention

Sequence 100 AA;

Query Match 66.0%; Score 163; DB 5; Length 100;
Best Local Similarity 70.8%; Pred. No. 7.7e-15; Indels 2; Gaps 1;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEVHHQKLVFPADGVGSKKISITIRIKGVIVRIETILF 48
DB 2 DAEFRHDSGYEVHHQKLVFPADGVGSKKISITIRIKGVIVRIETILF 47

RESULT 3
AAE14383
ID AAE14383 standard; protein; 108 AA.

AAE14383;

12-MAR-2002 (first entry)

Gamma-secretase substrate #5.

Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
APP; beta-secretase; Alzheimer's disease; fusion protein.

Unidentified.

Location/Qualifiers

1..100
/label= Beta-CTF_domain

Region 101..108
/note="Hydrophilic moiety"

MO200183811-A1.

08-NOV-2001.

25-APR-2001; 2001WO-US013332.

01-MAY-2000; 2000US-0201053P.

(MERI) MERCK & CO INC.

Li Y, Xu M, Huang Q, Gardell S;

WPI; 2002-066536/09.

Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.

Claim 8; Page 8; 36pp; English.

The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the
CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's

CC disease, and in the characterisation of the biological importance of
 CC gamma-secretase. The present sequence is an example of gamma-secretase
 CC substrate of the invention. The substrate is a fusion protein containing
 CC APP beta-CTF domain and a hydrophilic moiety

XX Sequence 108 AA;

Query Match 66.0%; Score 163; DB 5; Length 108;
 Best Local Similarity 70.8%; Pred. No. 8.5e-15;
 Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAERHDSGTVHOKLVFPAEDVGSNKKISTEIKGVIRIETILF 48
 |||||
 Db 2 DAERHDSGTVHOKLVFPAEDVGSNKKAIIGLWGVV--IATVIF 47

RESULT 4

AAR93556 AAR93556 standard; protein; 112 AA.

XX AAR93556;

DT 10-OCT-1996 (first entry)

XX Familial Alzheimer's disease APP isoform 751 fragment.

XX APP; amyloid precursor protein; isoform 751; inherent; familial;

KM Alzheimer's disease; mutation; diagnosis; transgenic model; study;

XX cognitive; beta A4 domain; exon 17; senility.

XX Homo sapiens.

Key Location/Qualifiers
 FT Domain 14..56
 /label=beta-A4_domain

FT Misc-difference 59
 /note="corresponds to bases 175-177 in file AAT18082, a
 TTC codon, this translation exception is the site of a
 Val to Ile mutation in isoform 751, bases 175-177
 probably should be ATC and not TTC"

PN M09606927-A1.

PD 07-MAR-1996.

PF 28-AUG-1995; 95MO-US010920.

PR 01-SEP-1994; 94US-00299872.

PA (MERI) MERCK & CO INC.

PI Singh G, Chen HY, Heavens RP, Sirinathsinghi DJ, Smith DW,
 PI Trumbauer MB, Van Der Ploeg LHT, Vongs A, Zheng H;

DR WPI; 1996-160358/16.

DR N-PSDB; AAT18082.

PT Transgenic animal expressing familial form of human amyloid precursor
 PT protein - used to evaluate compounds affecting Alzheimer's disease and
 PT other cognitive disorders.

XX Example 1; Fig 7; 32pp; English.

CC AAR93556 is a fragment of the amyloid precursor protein (APP) isoform 751
 CC from a patient diagnosed with familial Alzheimer's disease (FAD). The
 CC sequence given corresponds to amino acids 640-751 of FAD APP 751. A
 CC feature of FAD is a Val to Ile substitution at posn. 698 of the full APP
 CC (posn. 59 of this sequence). DNA encoding this sequence was used to
 CC construct expression vectors for the prodn. of transgenic animals (esp.
 CC mice) carrying the FAD APP 751 mutation. The transgenic animals are
 CC useful for the evaluation of test cpds. affecting Alzheimer's disease and
 CC other cognitive disorders and for identification of new targets in
 CC Alzheimer's disease since the progression of the disease can be followed

CC gradually. N.B. the V-I mutation at posn. 59 is given in the
 CC specification as being encoded by a TTC codon (most probably this should
 CC be ATC)

XX Sequence 112 AA;

Query Match 66.0%; Score 163; DB 2; Length 112;
 Best Local Similarity 70.8%; Pred. No. 8.9e-15;
 Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAERHDSGTVHOKLVFPAEDVGSNKKISTEIKGVIRIETILF 48
 |||||
 Db 14 DAERHDSGTVHOKLVFPAEDVGSNKKAIIGLWGVV--IATVIF 59

RESULT 5

AAW19484 AAW19484 standard; protein; 695 AA.

XX AAW19484;

DT 08-SEP-1997 (first entry)

XX APP695 mutant A-beta-containing protein.

XX Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;

XX APP.

XX Homo sapiens.

Key Location/Qualifiers
 FT Misc-difference 642
 /note="Wild-type Val is preferably substituted by Phe"

PN M09640895-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-US009679.

PR 07-JUN-1995; 95US-00486018.

PR 07-JUN-1995; 95US-00486538.

PA (ATRB-) ATHENA NEUROSCIENCES INC.

PI Mcconlogue LC, Seubert PA;

DR WPI; 1997-052308/05.

PT Transgenic mammal comprising DNA encoding A-beta-contg. protein - useful
 PT as animal model to test potential Alzheimer's disease treatments.
 XX Claim 11; Page; 116pp; English.

CC A novel non-human transgenic mammal has been produced which contains a
 CC nucleic acid construct for expression of A-beta- containing protein,
 CC stably incorporated into its genome. The construct comprises a promoter,
 CC for expression in a mammalian cell, operably linked to a region encoding
 CC the A-beta-containing protein, which includes amino acids 672-714 of
 CC human beta-amyloid precursor protein (APP), where the region is selected
 CC from DNA encoding the A-beta-containing protein consisting of all, or a
 CC contiguous portion of APP770, APP751 or APP695, or a mutant comprising a
 CC mutation in one or more of amino acids 669, 670, 671, 690, 692 and 717.
 CC The present sequence represents a mutant APP695 protein in which the
 CC codon encoding amino acid 717 is mutated from wild-type Val to Phe. The
 CC amino acid positions referred to in the specification are as they appear
 CC in APP770 (see AAW19482) i.e. position 717 represents position 642 in
 CC APP695, and 698 in APP751. The larger forms of APP (APP751, APP770)
 CC consist of APP695 plus one or two additional domains. The transgenic
 CC mammal is used as an animal model to test compounds for an effect on the
 CC expression or processing of an A-beta-containing protein, i.e. to test
 CC potential Alzheimer's disease treatments. N.B. The present sequence is
 CC shown in the specification, but has been derived from SEQ ID NO:2 which

Cc		is on pages 82-84
Xx		
Sq	Sequence 695 AA;	
	Query Match	66.0%; Score 163; DB 2; Length 695;
	Best Local Similarity	70.8%; Pred. No. 9.5e-14;
Matches	34; Conservative	4; Mismatches 8; Indels 2; Gaps 1
Dy	1 DAEPRHDSGYEVHHQKLVFPADYGSNKKISITELKGIVLHRIRLTIF 48 DABPFHDSDGYEVEHQKLVPFAPADYGSKAIIIGLMWGVV--IATVI 642	
Db	597 DAEPRHDSGYEVHHQKLVFPADYGSNKKISITELKGIVLHRIRLTIF 48	
	RESULT 6	
AAM19498		
ID	AAWI9498 standard; protein; 695 AA.	
XX	AAWI9498:	
AC		
XX	08-SEP-1997 (first entry)	
DT		
DE	APP695 mutant A-beta-containing protein.	
XX		
KM	Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein; APP.	
XX	Homo sapiens.	
O5		
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 642 /note= "Wild-type Val is preferably substituted by Phe"	
FN	WO9640896-A1.	
PB	19-DEC-1996.	
XX		
PE	07-JUN-1996; 96MO-USO09857.	
XX		
PR	07-JUN-1995; 95US-00480653.	
XX	(ATHENA) ATHENA NEUROSCIENCES INC.	
PA	Games KD, Schenk DB, McConlogue LC, Seubert PA, Rydel RB, MPI, 1997-052309/05.	
DR		
XX		
PT	Testing compounds for an effect on an Alzheimer's disease marker - uses non-human transgenic animals which can control expression of major forms of beta-amyloid precursor protein.	
FT		
PS	Claim 23; Page; 13pp; English.	
XX		
CC	A novel method has been produced for testing compounds for an effect on an Alzheimer's disease (AD) marker. The method involves administering the compound to be tested to a non-human transgenic mammal, or mammalian cells derived from the transgenic mammal, where the transgenic mammal has a nucleic acid construct stably incorporated into the genome which comprises a promoter for expression of the construct in a mammalian cell operably linked to a region encoding an A-beta-containing protein. The region is selected from DNA encoding the A-beta-containing protein consisting of all, or a contiguous portion of APP770, APP751 or APP695, or a mutant comprising a mutation in one or more of amino acids 669, 670, 671, 690, 692 and 717, which includes amino acids 672-714 of human beta-amyloid precursor protein (APP). The present sequence represents a mutanltic APP695 protein in which the codon encoding amino acid 717 is mutated (seecc features table). The amino acid positions referred to in the specification are as they appear in APP770 (see AAW19497) i.e. position 717 represents position 642 in APP695, and 698 in APP751. The larger forms of APP (APP751, APP770) consist of APP695 plus one or two additional domains. The method also involves detecting or measuring the AD marker such that any difference between the marker in the transgenic animal, or mammalian cells derived from the transgenic mammal, to which the compound has not been administered, is observed, where an observed	

CC	difference in the marker indicates that the compound has an effect on the
CC	marker. The transgenic animals, or cells are used to screen for compounds
CC	which alter the pathological course of AD as measured by their effect on
CC	the amount and/or histopathology of AD markers in animals as well as
CC	behavioural alterations. N.B. The present sequence is shown in the
CC	specification, but has been derived from SEQ ID NO:2 which is on pages
XX	103-105
SQ	Sequence 695 AA;
Query Match	66.0%; Score 163; DB 2; Length 695;
Best Local Similarity	70.8%; Pred. No. 9,5e-14;
Matches	34; Conservative 4; Mismatches 8; Indels 2; Gaps 1
Oy	1 DAEFRHDSGYEVHHQKLVFPADVDGNSKKISITEIKGIVRIEITILF 48 DB 597 DAEPFRHDSGYEVHHQKLVFPADVDGNSKKIGIAGVGV--LAVTIF 642
RESULT 7	
AAV88436	
ID	AAV88436 standard; protein; 695 AA.
AC	AAV88436;
DT	03-AUG-2000 (first entry)
DE	Human APP695-VF amino acid sequence.
KM	Aspartyl protease; aspartase; amyloid precursor protein; APP; App 2; Alzheimer's disease; beta secretase site; AEP695-VF.
OS	Homo sapiens.
PN	WO200017369-A2.
PD	30-MAR-2000.
PX	23-SEP-1999; 99WO-US020881.
PR	24-SEP-1998; 98US-0101594P.
PA	(PHRA) PHARMACIA & UPJOHN CO.
PI	Gurney ME, Bienkowski MJ, Heintzikon RL, Parodi LA, Yan R;
DR	WPI: 2000-303209/26. N-PSTDB; AAA15676.
PT	New enzyme designated human aspartase useful in research into Alzheimer's
PT	Disease is capable of cleaving amyloid protein precursor at the beta
PT	secretase site to produce amyloid beta peptide.
PS	Example 8; Page 131-135; 183pp; English.
XX	
XX	This sequence represents a modified version of the human amyloid
XX	precursor protein 695 (APP695) amino acid sequence. The sequence is used
XX	in an example of the invention, showing the activity of Hu-app2. The
XX	invention relates to a protease (e.g. Asp2) capable of cleaving the beta
XX	secretase site of amyloid precursor protein (APP). The protease contains
XX	a sequence encoding the amino acid sequence DTG and a sequence encoding
XX	DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
XX	causes an autosomal dominant form of Alzheimer's disease. APP localises
XX	to the cell surface membrane and have a single C-terminal transmembrane
XX	domain. Proteolytic processing of APP produces the amyloid beta protein,
XX	which is possibly very important in Alzheimer's disease. The invention
XX	includes a nucleotide sequence encoding the protease, a vector containing
XX	the nucleotide sequence, and a cell line comprising the vector. Methods
XX	for screening for inhibitors of beta secretase activity are also given in
XX	the invention. The human aspartase protein and nucleotide sequences and
XX	the methods for identifying inhibitors of the protease, are useful in the
XX	treatment of and research in to Alzheimer's disease

SQ Sequence 695 AA;

Query Match 66.0%; Score 163; DB 3; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14; Indels 2; Gaps 1;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFPAPEDVGSNKKISTIEIKGVYIRIETILF 48
|||||
D AEFRRHDSGYEVHHQKLVFPAPEDVGSNKKALIGLMVGCV--IATVIF 642

Db 597 DAEFRHDSGYEVHHQKLVFPAPEDVGSNKKALIGLMVGCV--IATVIF 642

RESULT 8

AAU07207
ID AAU07207 standard; protein; 695 AA.
XX
XX AAU07207;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human beta-amyloid protein precursor, APP695-VF.
DE
XX Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP695-VF.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 642
XX /note= "Wild type Val substituted by Phe"
XX
XX MO200149097-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001MO-IB000797.
XX
XX 09-MAY-2001; 2001MO-IB000797.
XX
XX (BIEN/) BIERKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
XX WPI; 2001-502548/55.
XX N-PSDB; AAS11707.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Example 8; Page 141-143; 185pp; English.

CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognizable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the

CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting hu-Asp
CC nucleic acids in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human amyloid
CC protein precursor, APP695-VF, the coding sequence of which was used to
CC prepare APP695-VF-KK (see AAS11710 and AAU07210) used in the method of
CC the invention
XX
XX

SQ Sequence 695 AA;

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14; Indels 2; Gaps 1;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFPAPEDVGSNKKISTIEIKGVYIRIETILF 48
|||||
D AEFRRHDSGYEVHHQKLVFPAPEDVGSNKKALIGLMVGCV--IATVIF 642

Db 597 DAEFRHDSGYEVHHQKLVFPAPEDVGSNKKALIGLMVGCV--IATVIF 642

RESULT 9

AAE10634
ID AAE10634 standard; protein; 695 AA.
XX
XX AAE10634;
XX
XX 10-DEC-2001 (first entry)
XX
XX Human amyloid protein precursor 695-VF (APP695-VF) isoform.
DE
XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP695-VF;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;
KW mutant; mutcin.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 642
XX /note= "Wild-type Val substituted with Phe"
XX
XX GB2357767-A.
XX
XX 04-JUL-2001.
XX
XX 22-SEP-2000; 2000GB-00023315.
XX
XX 23-SEP-1999; 99US-00404133.
XX 23-SEP-1999; 99US-0155493P.
XX 23-SEP-1999; 99WO-US020881.
XX 13-OCT-1999; 99US-00416901.
XX 06-DEC-1999; 99US-0169232P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Bienkowski MJ, Gurney M;
XX
XX WPI; 2001-444208/48.
XX N-PSDB; AAD17870.
XX
XX Polypeptide comprising fragments of human aspartyl protease with amyloid
XX precursor protein processing activity and alpha-secretase activity, for
XX identifying modulators useful in treating Alzheimer's disease.
XX
XX Example 8; Page 111-113; 187pp; English.

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity

CC Alzheimer's disease. The present sequence is human APP695-VF. This
 CC sequence is characterised by a V to F alteration at position 642
 XX

SO Sequence 695 AA;

Query Match 66.0%; Score 163; DB 4; Length 695;
 Best Local Similarity 70.8%; Pred. No. 9.5e-14;
 Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISITIKGVYVARITILP 48
 |||||
 DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKALIGLVGCV--IATVIF 642

RESULT 12

AA006608

ID AAU06608 standard; protein; 695 AA.

AC AAU06608;

DT 24-OCT-2001 (first entry)

DE Human Amyloid precursor protein mutant, APP695-VF.

XX Human; Aspartyl protease; Asp2b; beta-secretase; neurotropic;

KM neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KM amyloid-beta; Abeta; APP695-VF; London mutant; mutant; mutain.

XX Homo sapiens.

OS Homo sapiens.

Key Location/Qualifiers
 Misc-difference 642 /note="Wild-type Val substituted by Phe"

PN WO200149098-A2.

PD 12-JUL-2001.

XX 09-MAY-2001; 2001WO-IB000798.

XX 09-MAY-2001; 2001WO-IB000798.

XX (BIEN/) BIENKOWSKI M J.

PA (GURNEY/) GURNEY M B.

PA (HEIN/) HEINRIKSON R L.

PA (PARODI/) PARODI L A.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

DR WPI; 2001-502549/55.

XX N-PSDB; AAS11522.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity.

XX Example 8; Page 141-143; 185pp; English.

The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp proteins
 CC and vectors expressing them, and a polypeptide (isoform of amyloid
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or
 CC its fragment containing an APP cleavage site recognizable by a mammalian
 CC beta-secretase, and further comprising two lysine residues at the APP
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
 CC fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for

CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the APP-Sw-beta-secretase peptide sequence (NDA), which is
 CC associated with increased levels of Abeta processing is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridize to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is the human APP695 mutant, APP695-
 CC VF (the London mutation). The mutation alters the specificity of the APP
 CC gamma-secretase activity and increases the rate of processing of the
 CC amyloid Abeta peptide

SO Sequence 695 AA;

Query Match 66.0%; Score 163; DB 4; Length 695;
 Best Local Similarity 70.8%; Pred. No. 9.5e-14;
 Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISITIKGVYVARITILP 48
 |||||
 DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKALIGLVGCV--IATVIF 642

RESULT 13

AB078595

ID ABB78595 standard; protein; 695 AA.

AC ABB78595;

DT 16-JUL-2002 (first entry)

DE Human APP695-VF protein sequence SEQ ID NO.14.

XX Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;

KM amyloid precursor protein; APP.

XX Homo sapiens.

OS Homo sapiens.

PN GB2367060-A.

PD 27-MAR-2002.

XX 29-OCT-2001; 2001GB-00025934.

XX 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

PR 22-SEP-2000; 2000GB-00023315.

XX (PHAA) PHARMACIA & UPJOHN CO.

PA Bienkowski MJ, Gurney M;

PI WPI; 2002-397167/43.

XX N-PSDB; ABL52462.

XX Human aspartyl protease 1 substrates useful in assays to detect aspartyl

PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

PT Example 8; Page 111-113; 182pp; English.

The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the non

-coding strand complementary to a defined 1804 nucleotide sequence (see AB152456) where the nucleotide sequence encodes a polypeptide having Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane domain); (3) a purified polynucleotide (III') comprising a sequence that hybridizes under stringent conditions to (III) (the nucleotide sequence encodes a polypeptide further lacking a pro-peptide domain corresponding to amino acids 23-62 of hu-Asp1 (see AB178589)); (4) a vector (IV) comprising (III) or (III'); and (5) a host cell (V) transformed or transfected with (III), (III') and/or (IV). The hu-Asp1 protease substrate (I) may be used as an enzyme substrate in assays to detect aspartyl protease activity, (II) and therefore diagnose diseases associated with aberrant hu-Asp1 expression and activity such as Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present sequence represents human amyloid precursor protein APP695-VF, which is given in an example from the present invention

Query Match 66.0%; Score 163; DB 5; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKKISITBIKGYIVHRIETILF 48
DB 597 DAEFRHDSGYEVHOKLVFPADVGSNKKAIIGLVGGV--IATVIF 642

RESULT 14
AAY88430
ID AAY88430 standard; protein; 697 AA.

XX AAY88430;

DT 03-AUG-2000 (first entry)

XX Human APP695-VF-KK amino acid sequence.

XX Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KM Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX Homo sapiens.

XX MO200017369-A2.

XX 30-MAR-2000.

XX 23-SBP-1999; 99WO-US020881.

XX 24-SBP-1998; 98US-0101594P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;

XX MPI; 2000-303209/26.

DR N-PSDB; AAA15667.

PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.

XX Claim 133; Page 148-153; 183pp; English.

XX This sequence represents a modified version of the human amyloid
XX precursor protein (APP) amino acid sequence. The sequence is used in an
XX example of the method of the invention, to show that modification of APP
XX increases beta amyloid protein processing. The invention relates to a
XX protease (e.g. Asp2) capable of cleaving the beta secretase site of
XX amyloid precursor protein (APP). The protease contains a sequence
XX encoding the amino acid sequence DNG and a sequence encoding DSG or DNG
XX separated by 100-300 amino acids. When mutated the APP gene causes an
XX autosomal dominant form of Alzheimer's disease. APP localises to the cell

CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease

SQ Sequence 697 AA;

Query Match 66.0%; Score 163; DB 3; Length 697;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKKISITBIKGYIVHRIETILF 48
DB 597 DAEFRHDSGYEVHOKLVFPADVGSNKKAIIGLVGGV--IATVIF 642

RESULT 15

ID AAU07210 standard; protein; 697 AA.

XX AAU07210;

DT 24-OCT-2001 (first entry)

XX Human beta-amyloid protein precursor, APP695-VF-KK.

XX Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;

KM aspartyl protease 2; Asp2; amyloid protein precursor; APP;

XX beta-secretase; Alzheimer's disease; APP695-VF-KK.

XX Homo sapiens.

XX Location/Qualifiers

XX Key

XX Misc-difference 642 /note="Wild type Val substituted by Phe"

XX MO200149097-A2.

XX 12-JUL-2001.

XX 09-MAY-2001; 2001MO-1B000797.

XX 09-MAY-2001; 2001MO-1B000797.

XX (BIEN/) BIENKOWSKI M J.

XX (GURN/) GURNEY M E.

XX (HEIN/) HEINRIKSON R L.

XX (PARO/) PARODI L A.

XX (YANR/) YAN R.

XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX MPI; 2001-502548/55.

DR N-PSDB; AAS11710.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity.

XX Example 8; Page 150-152; 185pp; English.

XX The invention relates to a novel purified polypeptide comprising a
XX fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
XX Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
XX protein and the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. Also included is an isoform of amyloid protein precursor (APP)
XX comprising the amino acid sequence of a APP or its fragment containing an

CC APP cleavage site recognisable by a mammalian beta-secretase, and further
 CC comprising two lysine residues at the carboxyl terminus of the amino acid
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used
 CC for assaying for modulators of beta-secretase activity; identifying
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl
 CC protease (hu-Asp2); identifying agents that modulate the activity of Asp2
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
 CC Agents identified by the above methods are useful for treating
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta
 CC (Abeta) peptide production, for use in designing therapeutics for the
 CC treatment or prevention of Alzheimer's disease. Probes and primers
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The
 CC present sequence represents the amino acid sequence of human amyloid
 CC protein precursor, App695-VF-KK, used in the method of the invention
 XX

XX Sequence 697 AA;

Query Match 66.0%; Score 163; DB 4; Length 697;

Best Local Similarity 70.8%; Pred. No. 9.5e-14; Mismatches 8; Indels 2; Gaps 1;

Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 QY 1 DAEPFRHDSGYEVHOKLVFPADVGSNKKTSTIRKGVYHRIETILF 48
 DB 597 DAEPFRHDSGYEVHOKLVFPADVGSNKKALIGIMVGVV--IATVIF 642

Search completed: June 18, 2004, 19:58:53
 Job time : 70.2025 secs

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OM protein - protein search, using SW model

Run on: June 18, 2004, 19:54:46 ; Search time 18.8466 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-74

Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHOKLVF.....KISTIKGVIRITILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgm2_6/prodata/2/iaa/6A_COMB.pep:*
3: /cgm2_6/prodata/2/iaa/6B_COMB.pep:*
4: /cgm2_6/prodata/2/iaa/6C_COMB.pep:*
5: /cgm2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgm2_6/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	66.0	695	4	US-09-548-372D-14 Sequence 14, Appl
2	163	66.0	695	4	US-09-548-367D-14 Sequence 14, Appl
3	163	66.0	695	4	US-09-551-853D-14 Sequence 14, Appl
4	163	66.0	697	4	US-09-548-372D-20 Sequence 20, Appl
5	163	66.0	697	4	US-09-548-367D-20 Sequence 20, Appl
6	163	66.0	697	4	US-09-551-853D-20 Sequence 20, Appl
7	161.5	65.4	42	1	US-08-268-348A-6 Sequence 6, Appl
8	158.5	64.2	42	1	US-08-268-348A-5 Sequence 5, Appl
9	157.5	63.8	695	1	US-08-339-152A-30 Sequence 30, Appl
10	157	63.6	47	2	US-08-609-090-10 Sequence 10, Appl
11	157	63.6	48	4	US-09-560-883-11 Sequence 11, Appl
12	157	63.6	52	2	US-08-609-090-11 Sequence 11, Appl
13	157	63.6	53	3	US-09-173-887-5 Sequence 5, Appl
14	157	63.6	53	4	US-09-797-543-5 Sequence 5, Appl
15	157	63.6	59	1	US-08-484-969-3 Sequence 3, Appl
16	157	63.6	59	1	US-08-472-627-3 Sequence 3, Appl
17	157	63.6	59	1	US-08-388-463-3 Sequence 3, Appl
18	157	63.6	63	1	US-08-462-859A-4 Sequence 4, Appl
19	157	63.6	63	1	US-08-123-659A-4 Sequence 4, Appl
20	157	63.6	63	1	US-08-464-247A-4 Sequence 4, Appl
21	157	63.6	63	1	US-08-464-248A-4 Sequence 4, Appl
22	157	63.6	99	2	US-08-422-333-3 Sequence 3, Appl
23	157	63.6	99	3	US-08-339-708A-4 Sequence 4, Appl
24	157	63.6	99	3	US-08-339-708A-8 Sequence 8, Appl
25	157	63.6	100	6	Patent No. 5187153
26	157	63.6	100	6	Patent No. 5220013
27	157	63.6	100	6	Patent No. 5223482

28	157	63.6	103	2	US-08-404-831-2	Sequence 2, Appl
29	157	63.6	103	2	US-08-612-785B-2	Sequence 2, Appl
30	157	63.6	103	2	US-08-475-579A-2	Sequence 2, Appl
31	157	63.6	103	2	US-08-920-162A-2	Sequence 2, Appl
32	157	63.6	103	3	US-08-339-708A-10	Sequence 10, Appl
33	157	63.6	103	3	US-08-339-708A-12	Sequence 12, Appl
34	157	63.6	103	3	US-09-356-931-2	Sequence 2, Appl
35	157	63.6	103	4	US-08-703-675C-2	Sequence 2, Appl
36	157	63.6	103	4	US-08-617-267C-2	Sequence 2, Appl
37	157	63.6	103	4	US-09-519-019A-2	Sequence 2, Appl
38	157	63.6	105	2	US-08-729-345-1	Sequence 1, Appl
39	157	63.6	117	2	US-08-729-345-3	Sequence 3, Appl
40	157	63.6	117	4	US-09-422-569-10	Sequence 10, Appl
41	157	63.6	264	1	US-07-990-893-5	Sequence 5, Appl
42	157	63.6	487	1	US-08-462-859A-9	Sequence 9, Appl
43	157	63.6	487	1	US-08-123-659A-9	Sequence 9, Appl
44	157	63.6	487	1	US-08-464-247A-9	Sequence 9, Appl
45	157	63.6	487	1	US-08-464-248A-9	Sequence 9, Appl

ALIGNMENTS

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RESULT 1
US-09-548-372D-14
: Sequence 14, Application US/09548372D
: Patent No. 6420534
: GENERAL INFORMATION:
: APPLICANT: GUNNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: FILE REFERENCE: 29915/62801
: CURRENT APPLICATION NUMBER: US/09/548,372D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 695
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-548-372D-14
:
Query Match      66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 4e-15; Indels 2; Gaps 1;
Matches 34; Conservative 4; Mismatches 8;
Cy      1 DAEFRHDSGYEVHOKLVFAEDVGSNKKISTIKGVIRITILF 48
Db      597 DAEFRHDSGYEVHOKLVFAEDVGSNKKALIGLVGV--IATVIF 642

RESULT 2
US-09-548-367D-14
: Sequence 14, Application US/09548367D
: Patent No. 6440698
: GENERAL INFORMATION:
: APPLICANT: GUNNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: FILE REFERENCE: 29915/62808
: CURRENT APPLICATION NUMBER: US/09/548,367D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133

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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match
Best Local Similarity 70.8%; Score 163; DB 4; Length 697;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKISITTEIKGVIVHETLLE 48
Db 597 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKALIGLWGVV--IATVTF 642

RESULT 7
US-08-268-348A-6
Sequence 6, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Döbel, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-6

Query Match
Best Local Similarity 65.4%; Score 161.5; DB 1; Length 42;
Matches 32; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKISITTEIKGVIV 40
Db 1 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKALIGLWGVV 41

RESULT 8
US-08-268-348A-5
Sequence 5, Application US/08268348A
Patent No. 5750374
GENERAL INFORMATION:
APPLICANT: Döbel, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trotman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for Producing Hydrophobic
TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
TITLE OF INVENTION: Producing Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parise, John P.
REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-268-348A-5

Query Match
Best Local Similarity 64.2%; Score 158.5; DB 1; Length 42;
Matches 31; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKISITTEIKGVIV 40
Db 1 DAEFRHDSGYEVHQQKLVFFPAEDVGSNKKALIGLWGVV 41

RESULT 9
US-08-339-152A-30
Sequence 30, Application US/08339152A
Patent No. 5643726
GENERAL INFORMATION:
APPLICANT: Kovacs, Dora M.
APPLICANT: Tanzi, Rudolph E.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33

;; CORRESPONDENCE ADDRESS:
;; ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 New York Ave., NW, Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/339,152A
;; FILING DATE: 10-NOV-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Steffe, Eric K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 0609.4120000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 695 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-08-339-152A-30

Query Match 63.8%; Score 157.5; DB 1; Length 695;
Best Local Similarity 68.1%; Pred. No. 2.5e-14;
Matches 32; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISTEIKGVIVHRIETL 46
Db 597 DAEFRHDSGYEVHQLVFPADVGSNKKIIGLVGVIVATVI 643

RESULT 10
US-08-609-090-10
; Sequence 10, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARMY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-684-1111
;; TELEFAX: 703-684-1124
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 47 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-609-090-10

Query Match 63.6%; Score 157; DB 2; Length 47;
Best Local Similarity 70.2%; Pred. No. 9.2e-16;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISTEIKGVIVHRIETL 47
Db 1 DAEFRHDSGYEVHQLVFPADVGSNKKIIGLVGVIV--IATVI 45

RESULT 11
US-09-560-883-1
; Sequence 1, Application US/09560883
; Patent No. 6638711
; GENERAL INFORMATION:
; APPLICANT: Bush, Ashley
; APPLICANT: Huang, Xudong
; APPLICANT: Altwood, Craig
; APPLICANT: Tanzi, Rudolph
; TITLE OF INVENTION: Method of Screening for Drugs Useful in Treating Alzheimer's C
; FILE REFERENCE: 0609.4810001/RE/KKV
; CURRENT APPLICATION NUMBER: US/09/560,883
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/380,704
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04683
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 08/816,122
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Human amyloid protein precursor
; FEATURES:
; NAME/KEY: PEPTIDE
; LOCATION: (4)-(45)
; OTHER INFORMATION: A beta
; US-09-560-883-1

Query Match 63.6%; Score 157; DB 4; Length 48;
Best Local Similarity 70.2%; Pred. No. 9.5e-16;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISTEIKGVIVHRIETL 47
Db 4 DAEFRHDSGYEVHQLVFPADVGSNKKIIGLVGVIV--IATVI 48

RESULT 12
US-08-609-090-11
; Sequence 11, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARMY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

ADDRESS: LOMB PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-11

Query Match 63.6%; Score 157; DB 2; Length 52;
Best Local Similarity 70.2%; Pred. No. 1e-15;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHOKLVFPADVGSNNKISITIKGVIYHRIETIL 47
Db 1 DAEFRHDSGYEVHOKLVFPADVGSNNKAIIGLWVGIV--IATVI 45

RESULT 13
US-09-173-887-5
Sequence 5, Application US/09173887
Patent No. 6245884
GENERAL INFORMATION:
APPLICANT: Hook, Vivian Y. H.
TITLE OF INVENTION: SECRETSSES RELATED TO ALZHEIMER'S DEMENTIA
FILE REFERENCE: P-AS 3337
CURRENT APPLICATION NUMBER: US/09/173,887
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 53
TYPE: PRT
ORGANISM: mammalian
US-09-173-887-5

Query Match 63.6%; Score 157; DB 3; Length 53;
Best Local Similarity 70.2%; Pred. No. 1.1e-15;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHOKLVFPADVGSNNKISITIKGVIYHRIETIL 47
Db 4 DAEFRHDSGYEVHOKLVFPADVGSNNKAIIGLWVGIV--IATVI 48

RESULT 14
US-09-797-543-5
Sequence 5, Application US/09797543
Patent No. 6627409
GENERAL INFORMATION:
APPLICANT: Hook, Vivian Y. H.

TITLE OF INVENTION: SECRETSSES RELATED TO ALZHEIMER'S DEMENTIA
FILE REFERENCE: P-AS 4579
CURRENT APPLICATION NUMBER: US/09/797,543
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 09/173,887
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 53
TYPE: PRT
ORGANISM: 'Axial Seamount' polynoid polychaete
US-09-797-543-5

Query Match 63.6%; Score 157; DB 4; Length 53;
Best Local Similarity 70.2%; Pred. No. 1.1e-15;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHOKLVFPADVGSNNKISITIKGVIYHRIETIL 47
Db 4 DAEFRHDSGYEVHOKLVFPADVGSNNKAIIGLWVGIV--IATVI 48

RESULT 15
US-08-484-969-3
Sequence 3, Application US/08484969
Patent No. 5679531
GENERAL INFORMATION:
APPLICANT: Konig, Gerhard
APPLICANT: Graham, Paul
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSES: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,969
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: //label= Beta
OTHER INFORMATION: //note= "Beta cleavage site in APP"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: //label= Alpha
OTHER INFORMATION: //note= "Alpha cleavage site in APP, residues 16/17"

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OTHER INFORMATION: of BA4."
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in APP"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
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FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
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FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of APP"
US-08-484-969-3

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Query Match 63.6%; Score 157; DB 1; Length 59;
Best Local Similarity 70.2%; Pred. No. 1.2e-15;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

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QY 1 DAQFRHDSGVYVHOKLVFPADVGSNKKISITIKGVIVRIETIL 47
DB 5 DAQFRHDSGVYVHOKLVFPADVGSNKKAIIGLMGCVV--IATVI 49

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Search completed: June 18, 2004, 20:04:46
 Job time : 18.8466 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 18, 2004, 20:02:36 ; Search time 54.1841 Seconds
(Without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294a-74

Perfect score: 247
Sequence: 1 DAEFRHDSGYEVRHOKLVFPF.....KISITIKGVIRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 28213646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	100.0	48	US-09-865-294-74	Sequence 74, Appl
2	163	66.0	100	US-10-275-025-5	Sequence 5, Appl
3	163	66.0	108	US-10-275-025-13	Sequence 13, Appl
4	163	66.0	695	US-09-794-927-14	Sequence 14, Appl
5	163	66.0	695	US-09-795-847-14	Sequence 14, Appl
6	163	66.0	695	US-09-794-743-14	Sequence 14, Appl
7	163	66.0	695	US-09-794-748-14	Sequence 14, Appl
8	163	66.0	695	US-09-794-925-14	Sequence 14, Appl
9	163	66.0	695	US-09-861-442-14	Sequence 14, Appl
10	163	66.0	695	US-09-869-414-14	Sequence 14, Appl
11	163	66.0	695	US-09-548-366-14	Sequence 14, Appl
12	163	66.0	695	US-10-652-927-14	Sequence 14, Appl
13	163	66.0	695	US-10-652-830-14	Sequence 14, Appl
14	163	66.0	697	US-09-794-827-20	Sequence 20, Appl
15	163	66.0	697	US-09-795-847-20	Sequence 20, Appl

16	163	66.0	697	9	US-09-794-743-20	Sequence 20, Appl
17	163	66.0	697	9	US-09-794-748-20	Sequence 20, Appl
18	163	66.0	697	9	US-09-794-925-20	Sequence 20, Appl
19	163	66.0	697	9	US-09-681-442-20	Sequence 20, Appl
20	163	66.0	697	10	US-09-869-414-20	Sequence 20, Appl
21	163	66.0	697	10	US-09-548-366-20	Sequence 20, Appl
22	163	66.0	697	12	US-10-652-927-20	Sequence 20, Appl
23	163	66.0	697	12	US-10-652-830-20	Sequence 20, Appl
24	160	64.8	34	10	US-09-865-294-73	Sequence 73, Appl
25	157	63.6	53	9	US-09-797-543-5	Sequence 5, Appl
26	157	63.6	53	13	US-10-016-717-1	Sequence 14, Appl
27	157	63.6	70	9	US-09-155-076-14	Sequence 14, Appl
28	157	63.6	82	10	US-09-848-616-173	Sequence 173, App
29	157	63.6	82	14	US-10-050-902-219	Sequence 219, App
30	157	63.6	82	14	US-10-050-898-219	Sequence 219, App
31	157	63.6	99	14	US-10-183-119-2	Sequence 2, Appl
32	157	63.6	100	9	US-09-794-975-4	Sequence 4, Appl
33	157	63.6	100	15	US-10-275-025-1	Sequence 1, Appl
34	157	63.6	100	15	US-10-275-025-3	Sequence 3, Appl
35	157	63.6	100	15	US-10-275-025-4	Sequence 4, Appl
36	157	63.6	103	9	US-09-972-475-2	Sequence 2, Appl
37	157	63.6	103	9	US-09-895-443-2	Sequence 2, Appl
38	157	63.6	103	15	US-10-395-290-2	Sequence 2, Appl
39	157	63.6	103	15	US-10-463-729-2	Sequence 2, Appl
40	157	63.6	108	15	US-10-275-025-9	Sequence 9, Appl
41	157	63.6	108	15	US-10-275-025-11	Sequence 11, Appl
42	157	63.6	108	15	US-10-275-025-12	Sequence 12, Appl
43	157	63.6	117	9	US-09-794-975-6	Sequence 6, Appl
44	157	63.6	117	9	US-09-823-153-2	Sequence 2, Appl
45	157	63.6	117	10	US-09-422-569-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OR INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OR INVENTION: Prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 74
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Measles Virus
US-09-865-294-74

Query Match 100.0%; Score 247; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 5.1e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVRHOKLVFAEDGSKKISITIKGVIRIETILF 48
DB 1 DAEFRHDSGYEVRHOKLVFAEDGSKKISITIKGVIRIETILF 48

RESULT 2

US-10-275-025-5
; Sequence 5, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J
; TITLE OR INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO

```

; TITLE OF INVENTION: ASSAYS
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-CTF domain
US-10-275-025-5
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Query Match          66.0%; Score 163; DB 15; Length 100;
Best Local Similarity 70.8%; Pred. No. 2, 8e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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Qy      1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVIVHRIETILF 48
         |||||
Db      2 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV--IATVIF 47
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RESULT 3
US-10-275-025-13
; Sequence 13, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yuenming
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardelli, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gamma-secretase substrate
US-10-275-025-13
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Query Match          66.0%; Score 163; DB 15; Length 108;
Best Local Similarity 70.8%; Pred. No. 3e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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Qy      1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVIVHRIETILF 48
         |||||
Db      2 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV--IATVIF 47
```

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RESULT 4
US-09-794-927-14
; Sequence 14, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
```

```

Query Match          66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2, 7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
```

```

; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: US28
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280RC
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-14

Query Match          66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2, 7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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Qy      1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVIVHRIETILF 48
         |||||
Db      597 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV--IATVIF 642
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RESULT 5
US-09-795-847-14
; Sequence 14, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: US28
; FILE REFERENCE: 28341/6280RC
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-14
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```

Query Match          66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2, 7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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Db 597 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIIGLWGVV--IATVIF 642

RESULT 6

US-09-794-743-14
Sequence 14, Application US/09794743
Patent No. US20010021391A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND TITLE OF INVENTION: US95
FILE REFERENCE: 28341/6280BC
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-743-14

Query Match 66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 7

US-09-794-748-14
Sequence 14, Application US/09794748
Patent No. US20020037315A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND TITLE OF INVENTION: US95
FILE REFERENCE: 28341/6280BC
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-748-14

Query Match 66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Db 597 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIIGLWGVV--IATVIF 642

RESULT 8

US-09-794-925-14
Sequence 14, Application US/09794925
Patent No. US20020064819A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280H1
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-925-14

Query Match 66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Db 597 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIIGLWGVV--IATVIF 642

RESULT 9

US-09-681-442-14
Sequence 14, Application US/09681442
Patent No. US20020081634A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280FG
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24

CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-681-442-14

Query Match 66.0%; Score 163; DB 9; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVYVHRIETILF 48
DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKAIIGLWGVV--IATVIF 642

RESULT 10
US-09-869-414-14
Sequence 14, Application US/09869414
Publication No. US20030077226A1

GENERAL INFORMATION:
APPLICANT: Beinikowski et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280M
CURRENT APPLICATION NUMBER: US/09/869,414
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-869-414-14

Query Match 66.0%; Score 163; DB 10; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVYVHRIETILF 48
DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKAIIGLWGVV--IATVIF 642

RESULT 11
US-09-548-366-14
Sequence 14, Application US/09548366
Publication No. US20030104365A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Beinikowski, Michael J.

APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Ridiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
FILE REFERENCE: 28341/6280A
CURRENT APPLICATION NUMBER: US/09/548,366
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-366-14

Query Match 66.0%; Score 163; DB 10; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVYVHRIETILF 48
DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKAIIGLWGVV--IATVIF 642

RESULT 12
US-10-652-927-14
Sequence 14, Application US/10652927
Publication No. US20040043408A1
GENERAL INFORMATION:
APPLICANT: Gurney et al.
TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
FILE REFERENCE: 29915/6280N3
CURRENT APPLICATION NUMBER: US/10/652,927
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: 09/794,925
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 695
TYPE: PRT
ORGANISM: Homo sapiens
US-10-652-927-14

Query Match 66.0%; Score 163; DB 12; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGVYVHRIETILF 48
DB 597 DAEFRHDSGYEVHHQKLVFPADVGSNKKAIIGLWGVV--IATVIF 642

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OM protein - protein search, using SW model

Run on: June 18, 2004, 19:53:45 ; Search time 14.4294 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-74

Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISTEIKGVYHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	63.6	57	2 B60045	Alzheimer's disease
2	157	63.6	57	2 F60045	Alzheimer's disease
3	157	63.6	57	2 G60045	Alzheimer's disease
4	157	63.6	57	2 D60045	Alzheimer's disease
5	157	63.6	57	2 A60045	Alzheimer's disease
6	157	63.6	57	2 B60045	Alzheimer's disease
7	157	63.6	82	2 P00438	Alzheimer's disease
8	157	63.6	695	1 A49795	Alzheimer's disease
9	157	63.6	770	1 Q8HDA4	Alzheimer's disease
10	155	62.8	42	2 P05012	Alzheimer's disease
11	138	55.9	695	2 A27485	Alzheimer's disease
12	138	55.9	695	2 S00550	Alzheimer's disease
13	138	55.9	747	2 UH0773	Alzheimer's disease
14	133	53.8	33	2 S23094	Alzheimer's disease
15	64	25.9	546	1 VGNZRL	beta-amyloid prote
16	63.5	25.7	663	1 A86626	cell fusion glycop
17	62	25.1	327	2 S11435	hypothetical prote
18	62	25.1	662	1 VGNZCD	genome polyprotein
19	62	25.1	662	2 S21382	cell fusion glycop
20	61	24.7	546	2 S47300	gene F protein - r
21	61	24.7	631	1 VGNZPD	cell fusion glycop
22	61	24.7	631	1 A48346	cell fusion glycop
23	60	24.3	546	1 VGNZRX	cell fusion glycop
24	60	24.3	546	2 S55386	cell fusion protei
25	60	24.3	546	2 S47305	gene F protein - r
26	60	24.3	3063	2 JS0166	genome polyprotein
27	59	23.9	284	2 S04723	genome polyprotein
28	59	23.9	542	2 J02223	cell fusion protei
29	59	23.9	552	2 S47034	cell fusion protei

30	58	23.5	282	2 P00376	cell fusion glycop
31	58	23.5	282	2 P00388	cell fusion glycop
32	58	23.5	534	1 J00274	cell fusion glycop
33	58	23.5	550	1 A48556	cell fusion glycop
34	58	23.5	553	1 VGNZMV	cell fusion glycop
35	57	23.1	79	2 B90314	hypothetical prote
36	57	23.1	298	2 A90331	transposase in ISC
37	56.5	22.9	356	2 D96537	hypothetical prote
38	56.5	22.9	971	2 D70128	conserved hypothet
39	56	22.7	127	2 F90475	hypothetical prote
40	56	22.7	229	2 F86180	hypothetical prote
41	56	22.7	1328	2 B22999	YB protein - yeas
42	55.5	22.5	247	2 A85688	hypothetical prote
43	55.5	22.5	274	2 C90830	probable replicati
44	55.5	22.5	323	2 T14719	partitioning prote
45	55.5	22.5	330	2 A26205	coat protein precu

ALIGNMENTS

RESULT 1

B60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase ;

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13; Indels 2; Gaps 1;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISTEIKGVYHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKALIGLVGVV--IATVI 50

RESULT 2

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase ;

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13; Indels 2; Gaps 1;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISTEIKGVYHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKALIGLVGVV--IATVI 50

RESULT 3

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 4

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 5

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C/Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Query 1 DAEFRHDSGYEVHHQKLVFPADVGSNKKISTEIKGIVHRIETIL 47

DB 6 DAEFRHDSGYEVHHQKLVFPADVGSNKGAIIGLMVGVV--IATVI 50

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C/Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;

Best Local Similarity 70.2%; Pred. No. 3e-13;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 7

P00438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C/Accession: P00438; G60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A:Reference number: P00438; PMID:93075180; PMID:1445331

A:Accession: P00438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: GB:M8358; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 63.6%; Score 157; DB 2; Length 82;

Best Local Similarity 70.2%; Pred. No. 4.5e-13;

Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

RESULT 8

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A49795

R:Podlasky, M.B.; Jolan, D.R.; Selkoe, D.J.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; PMID:92017079; PMID:1656157

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117; PMID:1905180
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA51829.1; PID:9342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knutiz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 63.6%; Score 157; DB 1; Length 695;
 Best Local Similarity 70.2%; Pred. No. 4.5e-12;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

1 DAEFRDGGYGVHKKLVFPAEDVGSNKKISITIKVYHRTITL 47
 597 DAEFRDGGYGVHKKLVFPAEDVGSNKKIIGLVGVV--IATVI 641

RESULT 9

ORF004
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence, revision 28-Jul-1995 #text, change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A3360; A35486; I39452; I39451; I39453; I59562; A44
 4688; A28839; A23302; A60805; J10038; S06123; A60355; A59011; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Miltchaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The Pr44(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:69128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 A:Note: alternative splice form APP(695)
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360
 A:Note: alternative splice form APP(695)
 R:La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:69165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LNF>
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA313654.1; PID:9516074
 R:Johnstone, B.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, P.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:93392030; PMID:2675837
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Boes, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:9178613; PIDN:AA59502.1; PID:9178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLMPVPAPEAKYGR' <YOS2>
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AA59501.1; PID:9178615
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.U.; Power, M.D.; Lieberburg, I.; van Duin
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr
 A:Reference number: I39453; MUID:90260663; PMID:2111584
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
 A:Reference number: I59562; MUID:92022553; PMID:1925564
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MR>
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AA51991.1; PID:9236721
 R:Kamido, K.; Orr, H.T.; Payami, H.; Wajsbom, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson
 arakis, S.B.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:9305397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45155; NID:9257377; PIDN:AA523645.1; PID:9257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45156; NID:9257379; PIDN:AA523646.1; PID:9257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: sequence extracted from NCBI backbone (NCBI:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Greeschik, K.H.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
 A:Reference number: A03134; MUID:87144572; PMID:2861207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'R', 648-770 <ROB>
 A:Cross-references: GB:M6765; NID:9178539; PIDN:AAA51722.1; PID:9178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldberger, D.; Lerman, M.; McBride, O.W.; Saffioti, U.; Gajdaek, D.C.
 Science 235, 877-880, 1987

A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328; PMID:3810169
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M5553; NID:9178706; PIDN:AAA35540.1; PID:9178707
 A:Experimental source: brain
 R:Tanzi, R.B.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 225, 880-884, 1987
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329; PMID:2949367
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M5532; NID:9177957; PIDN:AAA51564.1; PID:9177958
 R:Dyckes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: 802638; MUID:88296437; PMID:2900137
 A:Accession: 802638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DVR>
 R:Tanzi, R.B.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640; PMID:2893290
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9293612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A>Note: alternative splice form APP(751)
 R:Porte, P.; Gonzalez-Dekhtit, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639; PMID:2893289
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:X00297; NID:928720; PIDN:CAA30050.1; PID:928721
 A>Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A28949; MUID:88122641; PMID:2893291
 A:Accession: A28949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9292611
 A:Experimental source: glioblastoma cell line
 A>Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three B
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: not compared with conceptual translation
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Molecule type: mRNA
 A:Accession: B30320
 A:Molecule type: not compared with conceptual translation
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, B.M.; Majocha, R.B.; Marotica, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954; PMID:2893379
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573
 A>Note: the authors translated the codon GAA for residue 599 as G1Y, ACC for residue 60
 8 as Val, GUG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
 A>Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Maeter, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martini, R.N.; Beyreuther, K
 Query Match 63.6%; Score 157; DB 1; Length 770;
 Best local similarity 70.2%; Pred. No. 5, 1e-12;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 QY 1 DAEFRDSCGYEVHOKLVFPADVGSNKKISTEIKGVVHILFTL 47
 |||||
 DB 672 DAEFRDSCGYEVHOKLVFPADVGSNKKAIIGLVGVV--IATVI 716
 |||||
 RESULT 10
 PN0512
 beta-amyloid protein - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: PN0512
 R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993
 A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein frag
 A:Reference number: PN0512; MUID:93290653; PMID:7685598
 A:Accession: PN0512
 A:Molecule type: protein
 A:Residues: 1-42 <SHI>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid
 Query Match 62.8%; Score 155; DB 2; Length 42;
 Best local similarity 77.5%; Pred. No. 3, 9e-13;
 Matches 31; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DAEFRDSCGYEVHOKLVFPADVGSNKKISTEIKGVIV 40
 |||||
 DB 1 DAEFRDSCGYEVHOKLVFPADVGSNKKAIIGLVGVV 40
 |||||
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A>Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec
 A:Reference number: A27485; MUID:88106489; PMID:3322280
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A>Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458; PMID:1756177
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Itami, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
 Gene 112, 189-195, 1992
 A>Title: Positive and negative regulatory elements for the expression of the Alzheimer
 A:Reference number: I49485; MUID:92209998; PMID:1555768
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RBS>

A:Cross-references: GB:D10603; NID:g220328; PIDN:BA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 55.9%; Score 138; DB 2; Length 695;
Best Local Similarity 63.8%; Pred. No. 1.2e-09;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 1 DA6FRHDSGYEVHROKLVFPAEDVGSNKISITEIKGVYHRIETIL 47
Db 597 DA6FRHDSGYEVHROKLVFPAEDVGSNKAIIGLMVGCV--IATVI 641

RESULT 12

S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SH1>
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA030488.1; PID:955617
R:Schubert, D.; Schroeder, R.; Lacomblere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: Protein
A:Residues: 18-37; 'X', 39-40; 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Heese, U.; Behner, D.; Maeters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempa, A.; Styles, J.; Mehra, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:623-648/Domain: transmembrane #status predicted <TM>

Query Match 55.9%; Score 138; DB 2; Length 695;
Best Local Similarity 63.8%; Pred. No. 1.2e-09;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 1 DA6FRHDSGYEVHROKLVFPAEDVGSNKISITEIKGVYHRIETIL 47
Db 597 DA6FRHDSGYEVHROKLVFPAEDVGSNKAIIGLMVGCV--IATVI 641

RESULT 13

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773

R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AA024853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 55.9%; Score 138; DB 2; Length 747;
Best Local Similarity 59.6%; Pred. No. 1.3e-09;
Matches 28; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Qy 1 DA6FRHDSGYEVHROKLVFPAEDVGSNKISITEIKGVYHRIETIL 47
Db 649 DSEYRHDYAVEVHROKLVFPAEDVGSNKAIIGLMVGCV--IATVI 693

RESULT 14

S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198; PMID:1618299
A:Accession: S23094
A:Molecule type: Protein
A:Residues: 1-93 <KO>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 53.8%; Score 133; DB 2; Length 33;
Best Local Similarity 89.3%; Pred. No. 2e-10;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DA6FRHDSGYEVHROKLVFPAEDVGSNK 28
Db 6 DA6FRHDSGYEVHROKLVFPAEDVGSNK 33

RESULT 15

VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N:Contains: fusion glycoprotein FL; fusion glycoprotein P2
C:Species: rinderpest virus
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: A28921
R:Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A:Title: Fusion glycoprotein (P) of rinderpest virus: entire nucleotide sequence of the
A:Reference number: A28921; MUID:88219541; PMID:3285575
A:Accession: A28921
A:Molecule type: mRNA
A:Residues: 1-546 <TSU>
A:Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-104/Product: cell fusion glycoprotein P2 #status predicted <FG2>
F:105-546/Product: cell fusion glycoprotein P1 #status predicted <FG1>
F:109-133/Domain: transmembrane #status predicted <TM1>
F:485-513/Domain: transmembrane #status predicted <TM2>
F:25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.9%; Score 64; DB 1; Length 546;

Mon Jun 21 11:39:13 2004

us-09-865-294a-74.rpr

Page 6

Best Local Similarity 61.1%; Pred. No. 3;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY      31 SITEIKGIVHRIETILF 48
        |::||| |||::|:::
DB      283 SLSEIKGIVHRLSVSY 300
```

Search completed: June 18, 2004, 20:03:31
Job time : 14.4294 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 9.42331 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-74
Sequence: 1 DABPRHDSGVVHHQKLVF.....KISTEIKGVVHLETLF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	157	63.6	57 1 A4 URDMA	Q29149 urens marit
2	157	63.6	58 1 A4 CANFA	Q28280 canis faml
3	157	63.6	58 1 A4 RABIT	Q28748 oryctolagus
4	157	63.6	58 1 A4 SHERP	Q28757 oris aries
5	157	63.6	59 1 A4 BOVIN	Q28053 bos taurus
6	157	63.6	751 1 A4 SAISC	Q95241 s amyloid b
7	157	63.6	770 1 A4 CAPO	Q60495 c amyloid b
8	157	63.6	770 1 A4 HUMAN	P05067 h amyloid b
9	157	63.6	770 1 A4 MACFA	P53601 m amyloid b
10	157	63.6	770 1 A4 PTG	P79307 s amyloid b
11	138	55.9	770 1 A4 MOUSE	P12023 m amyloid b
12	138	55.9	770 1 A4 RAT	P08592 r amyloid b
13	115	46.6	780 1 A4 TRTPL	O76883 tetradon f
14	111	44.9	737 1 A4 FUGRU	O93279 fugu rubrip
15	64	25.9	546 1 A4 POLG	P10864 rindipest
16	62	25.1	327 1 A4 POLG	P21294 potato vtru
17	62	25.1	662 1 A4 VGLF	P12569 canine dist
18	61	24.7	546 1 A4 VGLF	P41360 rindipest
19	61	24.7	631 1 A4 VGLF	P28886 plocine dis
20	60	24.3	546 1 A4 VGLF	P41356 rindipest
21	60	24.3	3063 1 A4 POLG	P18247 p genome po
22	59	23.9	284 1 A4 POLG	P11897 potato vtru
23	58	23.5	534 1 A4 VGLF	P26032 measles vir
24	58	23.5	550 1 A4 VGLF	P25973 measles vir
25	58	23.5	550 1 A4 VGLF	P08300 measles vir
26	57.5	23.1	506 1 A4 MATK	O47157 erica tetra
27	57	23.1	338 1 A4 SYFA	O84444 fusobacteri
28	56.5	22.9	356 1 A4 BCAG	O81246 borrelia bu
29	56.5	22.9	971 1 A4 V228	O81246 borrelia bu
30	56	22.7	229 1 A4 V726	O81246 borrelia bu
31	55.5	22.5	330 1 A4 COAT	O62991 rhododendro
32	55.5	22.5	330 1 A4 COAT	P07993 pepper molc
33	55.5	22.5	506 1 A4 MATK	O47143 calluna vul

34	55.5	22.5	1442 1	DPO3 URBPA	O96044 ureaplasma
35	55	22.3	220 1	V725 ARATH	O48850 arabidopsis
36	55	22.3	221 1	V714 ARATH	O94850 arabidopsis
37	55	22.3	240 1	V727 ARATH	O94850 arabidopsis
38	55	22.3	316 1	YMX1 CAEEL	P34509 caenorhabdi
39	54	21.9	321 1	R8SC ECOLI	P04584 escherichia
40	54	21.9	436 1	VGLF RINDK	P12574 rindipest
41	53.5	21.7	518 1	OPG3 NITEU	O94893 lactococcus
42	53.5	21.7	518 1	OPG3 NITEU	O94893 lactococcus
43	53.5	21.7	708 1	YN2B CAEEL	P45972 caenorhabdi
44	53.5	21.7	842 1	DP3A THEMA	O92594 thermotoga
45	53	21.5	251 1	TPIS_XANCP	O89700 xanthomonas

ALIGNMENTS

RESULT 1	A4 URDMA	STANDARD;	PRT;	57 AA.
AC	Q29149,			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog (Contains: Beta-amyloid protein (Beta-Ap4) (A-beta1) (Fragment).			
GN	APP.			
OS	Ursus maritimus (Polar bear) (Thalarchos maritimus).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Placentalia; Ursidae; Ursus.			
OX	NCBI_TaxID=29073;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RK	TISSUE=Brain;			
RC	MEDLINE=92017079; PubMed=1656157;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."			
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).			
CC	-1- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G10 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: Belongs to the APP family.			
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CC	EMBL: X56128; CAA39593.1; -.			
DR	PIR: B60045; B60045.			
DR	HSSP: P05067; IBA4.			
DR	InterPro: IPR008155; A4_APP.			
DR	InterPro: IPR001255; Beta-APP.			
DR	Pfam: PF03494; Beta-APP. 1.			
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.			
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.			
FT	NON_TER	1		
FT	CHAIN	1		
FT	DOMAIN	6	48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT	TRANSMEM	34	57	EXTRACELLULAR (POTENTIAL).
FT	NON_TER	57		POTENTIAL.
SQ	SEQUENCE	57 AA;	6172 MW;	84209088BA82DPA CRC64;
Query Match	63.6%;	Score 157;	DB 1;	Length 57;
Best Local Similarity	70.2%;	Pred. No. 1.4e-13;		
Matches	33;	Conservative	4;	Mismatches 8; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKISITEIKGVYHRIETIL 47
 DB 6 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKAIIGLAVGGV--IATYI 50

RESULT 2

AC 028280; STANDARD; PRT; 58 AA.

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-Ap) (A-beta)] (Fragment).
 GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]

SEQUENCE FROM N.A.

RP TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone B.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the APP family.

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DR EMBL; X56125; CAA39590.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49
 FT DOMAIN <1 34
 FT TRANSMEM 35 58
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2B12DFA CRC64;

Query Match 63.6%; Score 157; DB 1; Length 58;
 Best Local Similarity 70.2%; Pred. No. 1.5e-13;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKISITEIKGVYHRIETIL 47
 DB 7 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKAIIGLAVGGV--IATYI 51

RESULT 3

AC 028748; STANDARD; PRT; 58 AA.

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-Ap) (A-beta)] (Fragment).
 GN APP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]

SEQUENCE FROM N.A.

RP TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone B.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the APP family.

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DR EMBL; X56129; CAA39594.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48
 FT DOMAIN <1 33
 FT TRANSMEM 34 57
 FT DOMAIN 58 >58
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;

Query Match 63.6%; Score 157; DB 1; Length 58;
 Best Local Similarity 70.2%; Pred. No. 1.5e-13;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

OY 1 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKISITEIKGVYHRIETIL 47
 DB 6 DAEFRHDSGYEVHOKLVFFPAEDVGSNKKAIIGLAVGGV--IATYI 50

RESULT 4

AC 028757; STANDARD; PRT; 58 AA.

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 protein (Beta-Ap) (A-beta)] (Fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Heart;
 RA MEDLINE=92017079; PubMed=1656157;
 RT Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 CC EMBL; X56130; CAA39595.1; -;
 CC HSSP; P05067; IBA4.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC NON_TER 1
 CC CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 34 57 POTENTIAL.
 CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 CC NON_TER 58
 CC SEQUENCE 58 AA; 6300 MW; F434209D888BA82D CRC64;
 SQ
 Query Match 63.6%; Score 157; DB 1; Length 58;
 Best Local Similarity 70.2%; Pred. No. 1.5e-13;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKISITIKGVYHRIETLL 47
 DB 6 DAEFRHDSGYEVHOKLVFPAEDVGSNKALIGLWGVV--IATVI 50
 RESULT 5
 A4_BOVIN STANDARD; PRT; 59 AA.
 ID A4_BOVIN
 AC 026053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DR Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DR protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=92017079; PubMed=1656157;
 RA Johnstone B.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 CC EMBL; X56124; CAA39589.1; -;
 CC HSSP; P05067; IBA4.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR001255; Beta-APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 CC NON_TER 1
 CC CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 35 58 POTENTIAL.
 CC DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
 CC NON_TER 59
 CC SEQUENCE 59 AA; 6414 MW; F43469D488A2B12D CRC64;
 SQ
 Query Match 63.6%; Score 157; DB 1; Length 59;
 Best Local Similarity 70.2%; Pred. No. 1.5e-13;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 QY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKISITIKGVYHRIETLL 47
 DB 7 DAEFRHDSGYEVHOKLVFPAEDVGSNKALIGLWGVV--IATVI 51
 RESULT 6
 A4_SAISC STANDARD; PRT; 751 AA.
 ID A4_SAISC
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DR Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DR protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DR APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OC NCBI_Taxid=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Liver;
 RA MEDLINE=96108492; PubMed=8532114;
 RA Levy B., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy."
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to Apb1/Ttp60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).

Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metallothionein (CuMT) induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APPB family members, the APPA family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP1, APPB1, I81, KMS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAPK via the WT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=Additional isoforms seem to exist;

Name=APP770;

Isoid=G95241-1; Sequence=Displayed;

Name=APP695;

Isoid=G95241-2; Sequence=Not described;

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPXY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields Aβ peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

PTM: N- and O-glycosylated (By similarity).

CC	-1	PTM	Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).
CC	-1	MISCELLANEOUS	Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).
CC			Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).
CC	-1	SIMILARITY	Belongs to the APP family.
CC	-1	SIMILARITY	Contains 1 BPT1/Kunitz inhibitor domain.
CC			-----
CC			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or_send_an_email_to_license@isb-sib.ch).
CC			-----
DR		EMBL	S81024; AAD1347.1; -.
DR		HSSP	P05067; 1AAP.
DR		InterPro	IPR008155; A4_APP.
DR		InterPro	IPR008154; A4_extra.
DR		InterPro	IPR001255; Beta-APP.
DR		InterPro	IPR002223; Kunitz_BPT1.
DR		Pfam	PF02177; A4_EXTRA; 1.
DR		Pfam	PF03494; Beta-APP; 1.
DR		Pfam	PF00014; Kunitz_BPT1; 1.
DR		PRINTS	PR00203; AMYLOIDA4.
DR		PRINTS	PR00759; BASICPTASE.
DR		ProDom	PD000222; Kunitz_BPT1; 1.
DR		SMART	SM00006; A4_EXTRA; 1.
DR		SMART	SM00131; KU; 1.
DR		PROSITE	PS00319; A4_EXTRA; 1.
DR		PROSITE	PS00320; A4_INTRA; 1.
DR		PROSITE	PS00280; BPT_KUNITZ_1; 1.
DR		PROSITE	PS50279; BPT_KUNITZ_2; 1.
KW		Apoptosis	Endocytosis; Cell adhesion; Serine protease inhibitor;
KW		Coated pits	Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW		Zinc	Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW		Proteoglycan	Amyloid; Alternative splicing.
FT		SIGNAL	1..17
FT		CHAIN	18..751
FT		CHAIN	18..668
FT		CHAIN	18..652
FT		CHAIN	653..751
FT		CHAIN	653..694
FT		CHAIN	653..692
FT		CHAIN	653..751
FT		CHAIN	669..694
FT		CHAIN	669..692
FT		CHAIN	693..751
FT		CHAIN	695..751
FT		CHAIN	702..751
FT		CHAIN	721..751
FT		CHAIN	18..680
FT		TRANSMEM	681..704
FT		DOMAIN	705..751
FT		DOMAIN	96..110
FT		DOMAIN	181..188
FT		DOMAIN	291..341
FT		DOMAIN	316..344
FT		DOMAIN	363..428
FT		DOMAIN	504..521
FT		DOMAIN	713..732
FT		DOMAIN	230..260
FT		DOMAIN	274..280
FT		SITE	144..144
FT		ACT_SITE	301..302
FT		SITE	652..653
FT			CLEAVAGE (BY BETA-SECRETASE)

FT SITE 653 654 (BY SIMILARITY).
 FT SITE 668 669 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION
 FT SITE 687 687 INVOLVED IN OXIDATIVE REACTIONS
 FT SITE 692 693 INVOLVED IN OXIDATIVE REACTIONS
 FT SITE 694 695 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 FT SITE 705 715 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 FT SITE 720 721 BASOLATERAL SORTING SIGNAL
 FT SITE 738 741 CLEAVAGE (BY CASPASE-3, -6, -8 OR -9)
 FT SITE 740 743 ENDOCYTOSIS SIGNAL.
 NPXY MOTIF.
 Query Match 63.6%; Score 157; DB 1; Length 751;
 Best Local Similarity 70.2%; Pred. No. 2e-12;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DAHFRHDSGVYHOKLVFPADVDGNSKKISITEIKGVHRETTI 47
 DB 653 DAHFRHDSGVYHOKLVFPADVDGNSKKIIGLMGVV-IATVY 657

RESULT 7
 A4 CAVPO STANDARD; PRT; 770 AA.
 AC Q60495; Q60496; 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 NC NCB1_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RA "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOB.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RA "Isoform-specific effects of apolipoproteins B2, B3, and B4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;
 RA Beck M., Brunecker M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RA "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein.";

RL Neuroscience 95:243-254(2000).
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007;
 RA Plamix I., Masuhiro U., Tun H., Sridharan A., Golde T., Beckman C.,
 RA Zandi-Cherif C., Onstead L., Sambamurti K.;
 RA "A novel gamma-secretase assay based on detection of the putative
 RT C-terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPB1/Tipe60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC regulated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins B and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -1- FUNCTION: Amyloids elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPB
 CC family, MAP81P1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, IBL, KNS2
 CC (via its TPR domains), APPB2 (via BASS) and DPA1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOB, in vitro and in vivo. When lipidated,
 CC APOB3 appears to be the preferred amyloid binding isoform, while
 CC the APOB4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Comment-Additional isoforms, missing exons 7, 8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appcans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC -1- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are

predominantly expressed in peripheral organs such as muscle and liver.

-1- INDUCTOR: Increased levels during neuronal differentiation.

-1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue (by similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides. S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/alpha-secretin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTF8).

-1- PTM: Proteolytically cleaved by caspase-3 during neuronal apoptosis (by similarity).

-1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to the L-APP isoforms produces the APP proteoglycan core proteins, the apolipans (by similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific (by similarity).

Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins.

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (by similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates.

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: X97631; CAA66230.1; -
EMBL: X99198; CAA67589.1; -
HSPSP, P05067; 1BA4.
InterPro: IPR008155; A4_APP.
InterPro: IPR008154; A4_extra.
InterPro: IPR002223; Kunitz_BPTI.
Pfam: PF00014; Kunitz_BPTI. 1.
PRINTS: PR00759; AMYLOIDA4.
PRINTS: PR00759; BASICPTASR.
ProDom: PD000222; Kunitz_BPTI. 1.
SMART: SM00131; KJ. 1.
SMART: SM00139; A4_EXTRA. 1.
PROSITE: PS00320; A4_INTRA. 1.
PROSITE: PS00280; BPTI_KUNITZ_1. 1.
PROSITE: PS0279; BPTI_KUNITZ_2. 1.
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neurone; Hepatin-binding; Metal-binding; Copper; Iron; zinc; signal; Transmembrane; Glycoprotein; Phosphorylation;

KW Proteoglycan; Alternative splicing; Amyloid.
BY SIMILARITY.

FT	SIGNATURE	1	17	770
FT	CHAIN	18	667	AMYLOID BETA A4 PROTEIN.
FT	CHAIN	18	667	SOLUBLE APP-ALPHA (BY SIMILARITY).
FT	CHAIN	18	671	SOLUBLE APP-BETA (BY SIMILARITY).
FT	CHAIN	672	770	CTF-ALPHA (BY SIMILARITY).
FT	CHAIN	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT	CHAIN	672	713	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT	CHAIN	688	770	CTF-BETA (BY SIMILARITY).
FT	CHAIN	688	713	P3(42) (BY SIMILARITY).
FT	CHAIN	688	711	P3(40) (BY SIMILARITY).
FT	CHAIN	712	770	GAMMA-CTF(57) (BY SIMILARITY).
FT	CHAIN	714	770	GAMMA-CTF(57) (BY SIMILARITY).

Query Match 63.6%; DB 1; Length 770;
Best Local Similarity 70.2%; Pred. No. 2.1e-12;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

1 DAEFRDSCGYVHQTLVFEADVGSNKSTIRKGVVARIETLL 47
672 DAEFRDSCGYVHQTLVFEADVGSNKSTIRKGVVARIETLL 716

RESULT 8
A4_HUMAN STANDARD; PRT: 770 AA.
ID A4_HUMAN STANDARD; PRT: 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BFC38; Q9UC49; Q9UCB6; Q9UCB8; Q9UCD1; Q9Q058;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APP1) (PrelA) [contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (beta-APP42); Beta-amyloid protein 40 (beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (AID(57)); Gamma-CTF(50) (Gamma-
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
GN APP OR A4 OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Muehler-Hill B.,
RA "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RA cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88128427; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Han D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RA "A new A4 amyloid mRNA contains a domain homologous to serine
RA proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,
RA Unterbeck A., Beyreuther K., Muehler-Hill B.,
RA "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RA is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).

- [4]
SEQUENCE FROM N.A. (ISOFORM APP770).
MEDLINE=90236318; PubMed=2110105.
Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
Genomic organization of the human amyloid beta-protein precursor
gene.";
Gene 87:257-263(1990).
[5]
ERRATUM, AND REVISIONS.
Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;
Gene 102:291-292(1991).
[6]
SEQUENCE FROM N.A. (ISOFORM L-APP733).
TISSUE=Leukocyte;
MEDLINE=92568136; PubMed=1587857;
Koenig G., Moenning U., Czech C., Prior R., Banati R.,
Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
Identification and differential expression of a novel alternative
splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
leukocytes and brain microglial cells.";
J. Biol. Chem. 267:10804-10809(1992).
[7]
SEQUENCE FROM N.A. (ISOFORM APP770).
MEDLINE=97263807; PubMed=9108164;
Hattori M., Tanahara F., Furuhata Y., Tanahashi H., Hirose M.,
Saito M., Tsuchi S., Sasaki Y.;
A novel method for making nested deletions and its application for
sequencing of a 300 kb region of human APP locus.";
Nucleic Acids Res. 25:1802-1808(1997).
[8]
SEQUENCE FROM N.A. (ISOFORM APP639).
TISSUE=Brain;
MEDLINE=22744650; PubMed=12859342;
Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
Identification of a novel alternative splicing isoform of human
amyloid precursor protein gene, APP639.";
Eur. J. Neurosci. 18:102-108(2003).
[9]
SEQUENCE FROM N.A. (ISOFORM APP305).
TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932;
Straussberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschuler S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.B.,
Bromstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Holtzman E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.B.,
Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[10]
SEQUENCE OF 1-10 FROM N.A.
TISSUE=Liver;
MEDLINE=99016647; PubMed=3140222;
Schon E.A., Mita S., Sadlock J., Herbert J.;
A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
Nucleic Acids Res. 16:9351-9351(1988).
[11]
ERRATUM, AND REVISIONS.
Mita S., Sadlock J., Herbert J., Schon E.A.;
Nucleic Acids Res. 16:11402-11402(1988).
- [12]
SEQUENCE OF 1-75 FROM N.A.
MEDLINE=89165870; PubMed=2538123;
La Pauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
Characterization of the 5'-end region and the first two exons of the
beta-protein precursor gene.";
Biochem. Biophys. Res. Commun. 159:297-304(1989).
[13]
SEQUENCE OF 18-50.
TISSUE=Fibroblast;
MEDLINE=87250462; PubMed=3597385;
van Nostrand W.B., Cunningham D.D.;
Purification of protease nexin II from human fibroblasts.";
J. Biol. Chem. 262:8508-8514(1987).
[14]
PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
TISSUE=Brain;
MEDLINE=89346754; PubMed=2569763;
de Sauvage F., Octave J.N.;
A novel mRNA of the A4 amyloid precursor gene coding for a possibly
secreted protein.";
Science 245:651-653(1989).
[15]
PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
TISSUE=Brain;
MEDLINE=87231971; PubMed=3035574;
Robakis N.K., Ramakrishna N., Wolfe G., Winiowski H.M.;
Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and the neuritic plaque amyloid peptides.";
Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
[16]
SEQUENCE OF 286-366 FROM N.A.
MEDLINE=88122640; PubMed=2893290;
Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
Gusella J.F., Neve R.L.;
Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
Nature 331:528-530(1988).
[17]
SEQUENCE OF 287-367 FROM N.A.
MEDLINE=88122641; PubMed=2893291;
Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
Nature 331:530-532(1988).
[18]
SEQUENCE OF 507-770 FROM N.A.
TISSUE=Brain cortex;
MEDLINE=88124954; PubMed=2893379;
Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska B.M., Majocha R.B.,
Marotta C.A.;
Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
[19]
SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
MEDLINE=96139497; PubMed=8576160;
Behner D., Heese L., Masters C.L., Multhaup G.;
Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
J. Biol. Chem. 271:1613-1620(1996).
[20]
SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
AND AD GLY-717.
MEDLINE=93236601; PubMed=8476439;
Deman R.B., Rosenzwaig R., Miller D.L.;
A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
Biochem. Biophys. Res. Commun. 192:96-103(1993).
[21]
SEQUENCE OF 656-737 FROM N.A.
MEDLINE=89392030; PubMed=2675837;

RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris P.H.,
 RA Little S.P.;
 RA "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RT Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RL [121]

Query Match 63.6%; Score 157; DB 1; Length 770;
 Best Local Similarity 70.2%; Pred. No. 2, 1e-12;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRDSDGYEVHOKLVFADVGSNKKISITIKGVYHRIETL 47
 DB 672 DAEFRDSDGYEVHOKLVFADVGSNKKAIIGLWGVV--IATYI 716

RESULT 9
 A4_MACPA STANDARD; PRT; 770 AA.
 ID AC P53601: 095K0N7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 amyloid beta protein homology) [Contains: Soluble APP-alpha (S-APP-alpha);
 Soluble APP-beta (S-APP-beta) : C99; Beta-amyloid protein 42 (Beta-
 APP42) Beta-amyloid protein 40 (Beta-APP40) : C83; P3(42), P3(40);
 Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 secretase C-terminal fragment 50); C31].
 GN APP.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CC NCB1_TaxID=9541;
 RN [1]
 RP TISSUE=Cerebellum;
 RC TISSUE=Cerebellum;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlinsky M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease.";
 RL Am. J. Pathol. 138:1423-1435(1991).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPT domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transition metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding

CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein APP, PPT1, APPBP1, IBI, KNS2
 CC (via its TPR domain) (By similarity). APPB2 (via BASS) and DBP1.
 CC In vitro, it binds MAP7 via the WT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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cytoplasmic proteins, including APPB family members, the APPA family, MAPKIP1, and SHC1. Numb and Dab1 (by similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, PEPPL, APPB1, IBI, KNS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAP1 via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptide. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

- PTM: N- and O-glycosylated (By similarity).

- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

- SIMILARITY: Belongs to the APP family.

- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL, AB032550; BAA84580.1; -

DR EMBL: Z84022; CAB06313.1; -
 DR EMBL: X56127; CAA39592.1; -
 DR HSPB, P05067; 1AAB.
 DR InterPro: IPR008155; A4_APP.
 DR InterPro: IPR008154; A4_extra.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; K2; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_2; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 DR Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurons; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 KM SIGNAL.
 FT CHAIN 1 17
 FT CHAIN 18 770
 FT CHAIN 18 687
 FT CHAIN 18 671
 FT CHAIN 672 770
 FT CHAIN 672 713
 FT CHAIN 672 770
 FT CHAIN 688 770
 FT CHAIN 688 713
 FT CHAIN 688 711
 FT CHAIN 712 770
 FT CHAIN 714 770
 FT CHAIN 721 770
 FT CHAIN 740 770
 FT CHAIN 740 699
 FT CHAIN 723 770
 FT TRANSMEM 724 770
 FT DOMAIN 96 110
 FT DOMAIN 135 155
 FT DOMAIN 181 188
 FT DOMAIN 291 341
 FT DOMAIN 391 423
 FT DOMAIN 491 522
 FT DOMAIN 523 540
 FT DOMAIN 732 751
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT ACT SITE 301 302
 FT SITE 671 672
 FT SITE 672 673
 FT SITE 687 688
 FT SITE 704 704
 FT SITE 706 706
 FT SITE 711 712
 FT SITE 713 714
 FT SITE 720 721

Query Match 63.6%; Score 157; DB 1; Length 770;
 Best Local Similarity 70.2%; Pred. No. 2, 1e-12;
 Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 DB 1 DAEPRDSDGYVHHQGLVFPADVGSNKKCSITEIKGVVHRIETLL 47
 672 DAEPRDSDGYVHHQGLVFPADVGSNKKATIGLWGVV--IATVI 716

RESULT 11
 A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023; P97487; P97942; G99K32;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease
 amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains:
 Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
 (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CRF(59) (Gamma-secretase
 C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C59); Gamma-CRF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CRF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 50) (AID(50)); C31).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280.
 RA Yamada T., Sasaki H., Futaya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leeuwen F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=GAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RT Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209988; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RT Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallegange D.B.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN RP SEQUENCE OF 281-380 FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain; and Kidney;
 RX MEDLINE=89149813; PubMed=2493250.
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblatt K., Capocchi M.,
 RT Loring J.P., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-I.";
 RL Neuron 28:449-459(2000).
 RN RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743, TYR-757, ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Nishikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
 RT scaffold Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189;
 RA Tarru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN RP

INTERACTION OF CTF PEPTIDES WITH NUMB.
 MEDLINE=22008109; PubMed=12011466;
 Roncarati R., Seelan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 Meucci O., McGrade J.C., Rakic P., D'Adamo L.;
 "The gamma-secretase-generated intracellular domain of beta-amyloid
 precursor protein binds Numb and inhibits Notch signaling.";
 Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 (13)
 GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APPB1.
 MEDLINE=21437805; PubMed=11553691;
 Cupere P., Orleans I., Craessaerts K., Annaert W., De Strooper B.;
 "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 gamma-secretase is rapidly degraded but distributes partially in a
 nuclear fraction of neurons in culture.";
 J. Neurochem. 78:1168-1178(2001).
 -1- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell mobility and transcription regulation through protein-protein
 interactions. Can promote transcription activation through binding
 to APB1/Tip60 and inhibit Notch signaling through interaction
 with Numb. Couples to apoptosis-inducing pathways such as those
 mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
 similarity). Acts as a kinesin I membrane receptor, mediating the
 axonal transport of beta-secretase and presenilin 1. May be
 involved in copper homeostasis/oxidative stress through copper ion
 reduction. Can regulate neurite outgrowth through binding to
 components of the extracellular matrix such as heparin and
 collagen I and IV (By similarity). The splice isoforms that
 contain the BPTI domain possess protease inhibitor activity (By
 similarity).
 -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as
 copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 only weakly transient metals and have little reducing activity due
 to substitutions of transient metal chelating residues. Beta-APP42
 may activate mononuclear phagocytes in the brain and elicit
 inflammatory responses. Promotes both tau aggregation and TPK II-
 mediated phosphorylation (By similarity).
 -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 peptides, including C31, are potent enhancers of neuronal
 apoptosis.
 -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 cytoplasmic proteins, including APPB family members, the APPA
 family, MAPKIP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 its serine phosphorylation. Also interacts with GPCR-like protein
 BPP1, FPR1, APPB1, IBL, KNS2 (via its TPR domains), APPB2 (via
 BASS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 MT-binding domains (By similarity). Associates with microtubules
 in the presence of ATP and in a kinesin-dependent manner (By
 similarity). Interacts, through a C-terminal domain, with GNAO1
 (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 neurons (By similarity). Beta-amyloid associates with HAH2 (By
 similarity).
 -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 protein that rapidly becomes internalized via clathrin-coated
 pits. During maturation, the immature APP (N-glycosylated in the
 endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 55.9%; Score 138; DB 1; Length 770;
 Best Local Similarity 63.8%; Pred. No. 5; 8-10;
 Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;
 1 DAEFHDSGYVHQLVFPADVGSKKISTIEIKGVHRIETL 47
 DB 672 DAEFGHDSGFVHQLVFPADVGSKKAIIGLWGVV--IATVI 716

RESULT 12
 A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)

01-DEC-1992 (Rel. 24, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble
 APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
 amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
 C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
 fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
 Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
 GN
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 in rat brain suggests a role in cell contact.";
 EMBO J. 7:1365-1370(1988).
 RN
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 Nucleic Acids Res. 17:2130-2130(1989).
 RN
 RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
 RX MEDLINE=2143797; PubMed=1148358;
 RA Gu Y., Misonou H., Sato T., Dohme N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 family resembling gamma-secretase-like cleavage of Notch.";
 J. Biol. Chem. 276:35235-35238(2001).
 RN
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandriuk R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 isoforms.";
 Ann. N.Y. Acad. Sci. 777:281-287(1996).
 RN
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=95263526; PubMed=7744833;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vasiliacopoulos D.,
 Mytilineou C., Margolis R.U., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 brain and is produced by astrocytes but not by neurons in primary
 neural cultures.";
 J. Biol. Chem. 270:11839-11844(1995).
 RN
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=97150061; PubMed=8996834;
 RA Sandriuk R., Morning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 and aging.";
 Gerontology 43:119-131(1997).
 RN
 RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
 TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
 Suzuki T., Naito A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DB1) binds to the cytoplasmic domain of the
 Alzheimer's amyloid precursor protein.";
 J. Neurochem. 72:549-556(1999).
 RN
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024358;
 RA Brouillet B., Tremblau A., Gailanaud D., Volovitch M., Brouillet C.,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 46.5276 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-74

Perfect score: 247
Sequence: 1 DA6FRHDSGYEVHKKLVF.....KISITRIKVIYRITILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	163	66.0	82	4 Q16014	Q16014 homo sapien
2	157	63.6	82	4 Q16020	Q16020 homo sapien
3	157	63.6	82	4 Q16019	Q16019 homo sapien
4	157	63.6	113	13 Q8JH58	Q8JH58 chelydra se
5	157	63.6	534	13 Q93296	Q93296 gallus gall
6	157	63.6	695	13 Q9DCJ8	Q9DCJ8 gallus gall
7	157	63.6	751	13 Q9DCJ7	Q9DCJ7 gallus gall
8	156.5	63.4	569	13 Q9PVL1	Q9PVL1 gallus gall
9	152	61.5	30	4 Q9UCA9	Q9UCA9 homo sapien
10	152	61.5	33	4 Q9UCJ3	Q9UCJ3 homo sapien
11	147	59.5	28	4 Q9UCD1	Q9UCD1 homo sapien
12	138	55.9	79	11 Q35463	Q35463 cricetus
13	138	55.9	218	11 Q8BPP5	Q8BPP5 mus musculu
14	138	55.9	384	11 Q8BPC7	Q8BPC7 mus musculu
15	138	55.9	693	13 Q98SG0	Q98SG0 xenopus lae
16	138	55.9	747	13 Q91963	Q91963 xenopus. ap

17	135	54.7	695	13 Q98SF9	Q98SF9 xenopus lae
18	135	54.7	695	13 Q7ZXQ0	Q7ZXQ0 xenopus lae
19	128	51.8	699	13 Q57394	Q57394 narke japon
20	106	42.9	19	4 Q9UCJ8	Q9UCJ8 homo sapien
21	98.5	39.9	357	13 Q8UUI8	Q8UUI8 brachydantio
22	98.5	39.9	472	13 Q8UUS0	Q8UUS0 brachydantio
23	98.5	39.9	612	13 Q919E7	Q919E7 brachydantio
24	98.5	39.9	678	13 Q7ZZT1	Q7ZZT1 brachydantio
25	98.5	39.9	738	13 Q90WZ8	Q90WZ8 brachydantio
26	96	38.9	239	13 Q8UUI7	Q8UUI7 brachydantio
27	96	38.9	694	13 Q8UUR9	Q8UUR9 brachydantio
28	95	38.5	35	4 Q8WZ99	Q8WZ99 homo sapien
29	63.5	25.7	663	16 Q9CJ14	Q9CJ14 lactococcus
30	62	25.1	365	12 Q9WC05	Q9WC05 potaro viru
31	62	25.1	528	12 Q9YJW9	Q9YJW9 canine dist
32	62	25.1	662	12 Q9DXZ2	Q9DXZ2 canine dist
33	62	25.1	662	12 Q9YKJ7	Q9YKJ7 canine dist
34	62	25.1	662	12 Q893Z7	Q893Z7 canine dist
35	61	24.7	49	6 Q97917	Q97917 bos taurus
36	61	24.7	546	12 Q91HA5	Q91HA5 rinderpest
37	60	24.3	508	8 Q8W7S3	Q8W7S3 ternstroemi
38	60	24.3	508	8 Q8W7S2	Q8W7S2 ameslea fir
39	60	24.3	546	12 Q849Z6	Q849Z6 peste-des-p
40	60	24.3	662	12 Q91KN3	Q91KN3 canine dist
41	60	24.3	3063	12 Q8JQ05	Q8JQ05 potaro viru
42	59	23.9	292	12 Q85Z76	Q85Z76 potaro viru
43	59	23.9	332	12 Q9DQNS	Q9DQNS potaro viru
44	59	23.9	337	12 Q8UPW2	Q8UPW2 potaro viru
45	59	23.9	530	12 Q8QV06	Q8QV06 canine dist

ALIGNMENTS

RESULT 1

ID Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014

DT 01-NOV-1996 (TRENBLER. 01, Created)

DT 01-NOV-1996 (TRENBLER. 01, Last sequence update)

DT 01-JUN-2003 (TRENBLER. 24, Last annotation update)

DB Beta-amyloid peptide (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9323601; PubMed=8476439;

RA Denman R.B., Rosenzweig R., Miller D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

RT mutations on the processing of the beta-amyloid peptide precursor."

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; AAB26263.2; -

DR HSSP; P05067; IBA4.

DR GO; GO:0016020; C:membrane; IBA.

DR InterPro; IPR001255; Beta-ApP.

DR Pfam; PF03494; Beta-ApP; 1.

FT NON_TER 1

FT NON_TER 82

SO SEQUENCE 82 AA; 8972 MW; F534AC5B3EA9230A CRC64;

Query Match 66.0%; Score 163; DB 4; Length 82;

Best Local Similarity 70.8%; Pred. No. 8.2e-14;

Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DA6FRHDSGYEVHKKLVFPAEDVGSNNKISITRIKVIYRITILF 48

Db 18 DA6FRHDSGYEVHKKLVFPAEDVGSNNKISITRIKVIYRITILF 63

RESULT 2

Q16020

ID 016020 PRELIMINARY; PRT: 82 AA.
AC 016020:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 82 AA; 8882 MW; P534AA5AE5D9230A CRC64;

Query Match 63.6%; Score 157; DB 4; Length 82;
Best Local Similarity 70.2%; Pred. No. 5.1e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISITIKGVVHRIETLL 47
Db 18 DAEFRHDSGYEVHQLVFPADVGSNKGAIIGLWGVV--IATVI 62
RESULT 3
Q16019 PRELIMINARY; PRT: 82 AA.
ID 016019:
AC 016019:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 82 AA; 8938 MW; P534AA50B579230A CRC64;

Query Match 63.6%; Score 157; DB 4; Length 82;
Best Local Similarity 70.2%; Pred. No. 5.1e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISITIKGVVHRIETLL 47
Db 18 DAEFRHDSGYEVHQLVFPADVGSNKGAIIGLWGVV--IATVI 62

RESULT 4
ID 08UH58 PRELIMINARY; PRT: 113 AA.
AC 08UH58:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amyloid beta protein (Fragment).
GN Chelydra serpentina (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Ocylphenol (OP) alters the expression of members of the amyloid
protein family in the hypothalamus of the snapping turtle, Chelydra
serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4 APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 63.6%; Score 157; DB 13; Length 113;
Best Local Similarity 70.2%; Pred. No. 7.3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
Qy 1 DAEFRHDSGYEVHQLVFPADVGSNKKISITIKGVVHRIETLL 47
Db 15 DAEFRHDSGYEVHQLVFPADVGSNKGAIIGLWGVV--IATVI 59

RESULT 5
ID 093296 PRELIMINARY; PRT: 534 AA.
AC 093296:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amyloid protein (Fragment).
GN Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER
FT NON_TER

```

SQ  SEQUENCE 534 AA; 60597 MW; FBS3BEC2866D4C92 CRC64;
  Query Match 63.6%; Score 157; DB 13; Length 534;
  Best Local Similarity 70.2%; Pred. No. 4, 2e-12;
  Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Cy 1 DAEPRHDSGYEVHHQKLVFPADVGSNNKKISITRKGYIVHRIETIL 47
   |||||
Db 436 DAEPRHDSGYEVHHQKLVFPADVGSNNKGAIIGLWVGIV--IATVI 480

RESULT 6
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
  isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 63.6%; Score 157; DB 13; Length 695;
Best Local Similarity 70.2%; Pred. No. 5, 7e-12;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Cy 1 DAEPRHDSGYEVHHQKLVFPADVGSNNKKISITRKGYIVHRIETIL 47
   |||||
Db 597 DAEPRHDSGYEVHHQKLVFPADVGSNNKGAIIGLWVGIV--IATVI 641

RESULT 7
ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
  isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -.

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Query Match	Score	DB	Length	669
Beat Local Similarity	68.1%	Pred. No. 5.3e-12;		
Matches	32; Conservative	4; Mismatches	10; Indels	1; Gaps

Query Match	Score	DB	Length	751
Beat Local Similarity	63.6%	Pred. No. 6.2e-12;		
Matches	33; Conservative	4; Mismatches	8; Indels	2; Gaps

Query Match	Score	DB	Length	697
Beat Local Similarity	63.4%	Pred. No. 5.3e-12;		
Matches	32; Conservative	4; Mismatches	10; Indels	1; Gaps

```
RESULT 9
Q9UC33 PRELIMINARY; PRT; 30 AA.
ID 09UC33;
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 13, Last sequence update)
DE Beta-amyloid protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28

RESULT 10
Q9UC33 PRELIMINARY; PRT; 33 AA.
ID 09UC33;
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sima S., Schlossmacher M., Whaley J., Swindlerst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28

RESULT 11
Q9UC33
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ID 09UCD1 PRELIMINARY; PRT; 28 AA.
AC 09UCD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RL J. Neurochem. 61:1965-1968(1993).
DR HSSP; P05067; 1AMB.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSN 27
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSN 27

RESULT 12
Q35463 PRELIMINARY; PRT; 79 AA.
ID 035463;
AC Q35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR030413; AAB86608.1; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 79
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 3JF2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 63.8%; Pred. No. 1.6e-10;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 47
DB 21 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 47

RESULT 13
Q8BPV5 PRELIMINARY; PRT; 218 AA.
ID Q8BPV5;
AC Q8BPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DB Amyloid beta (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK052448; BAC34997.1; -.
DR MGD; MGI:88059; App.
DR GO; GO:0005515; P:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR Pfam; PF03494; Beta-APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95855AFDAE1D0E65 CRC64;

Query Match 55.9%; Score 138; DB 11; Length 218;
Best Local Similarity 63.8%; Pred. No. 5e-10;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKKISTIKGVVHRIETLL 47
DB 120 DAEFRHDSGYEVHOKLVFPADVGSNKKAIIGLWVGTV--IATVI 164

RESULT 14

ID Q8BPC7 PRELIMINARY; PRT; 384 AA.
AC Q8BPC7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DB Amyloid beta (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK076506; BAC36369.1; -.
DR MGD; MGI:88059; App.
DR GO; GO:0005515; P:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 384 AA; 43990 MW; A81BAD8AE683173 CRC64;

Query Match 55.9%; Score 138; DB 11; Length 384;
Best Local Similarity 63.8%; Pred. No. 9.4e-10;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKKISTIKGVVHRIETLL 47
DB 286 DAEFRHDSGYEVHOKLVFPADVGSNKKAIIGLWVGTV--IATVI 330

RESULT 15
ID Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DB Beta-amyloid precursor protein A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Theis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
RL EMBL; AJ298150; CAC37193.1; -.
DR HSP; P05067; IHz3.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL 1
SQ SEQUENCE 693 AA; 78568 MW; CAP1DE655CLA653 CRC64;

Query Match 55.9%; Score 138; DB 13; Length 693;
Best Local Similarity 59.6%; Pred. No. 1.8e-09;
Matches 28; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

QY 1 DAEFRHDSGYEVHOKLVFPADVGSNKKISTIKGVVHRIETLL 47
DB 595 DAEFRHDSGYEVHOKLVFPADVGSNKKAIIGLWVGTV--IATVI 639

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